

Access DB# 97681

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
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STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4446</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>6/30/03</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>6/30/03</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>2</u>	Other _____	Other (specify) _____

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GenScore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: June 29, 2003, 14:00:00 / Search time: 11 seconds

(without alignment)
1267.031 Million cells 254865/sec

Title: US-09-905-744b-6

Perfect score: 428

Sequence: 1 WATERWATERWATERWATER

Scoring table:

Gap: 60.0, Gapext: 60.0

Searched: 119900 seqs, 4147023 residues

Word size: 3

Total number of hits satisfying chosen parameters: 119900

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: filtering filter 100 similarities

Database: SwissProt_40.4

Prod. No. is the number of protein profiles used by CompuGen Ltd.
Score greater than 1.0 indicates the score of the protein being filtered,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query	Length	DB ID	Description
1	408	100.0	100	EM22_HUMAN	EM22_HUMAN
2	407	100.0	100	EM22_HUMAN	EM22_HUMAN
3	407	100.0	100	EM22_HUMAN	EM22_HUMAN
4	407	100.0	100	EM22_HUMAN	EM22_HUMAN
5	407	100.0	100	EM22_HUMAN	EM22_HUMAN
6	407	100.0	100	EM22_HUMAN	EM22_HUMAN
7	407	100.0	100	EM22_HUMAN	EM22_HUMAN
8	407	100.0	100	EM22_HUMAN	EM22_HUMAN
9	407	100.0	100	EM22_HUMAN	EM22_HUMAN
10	407	100.0	100	EM22_HUMAN	EM22_HUMAN
11	407	100.0	100	EM22_HUMAN	EM22_HUMAN
12	407	100.0	100	EM22_HUMAN	EM22_HUMAN
13	407	100.0	100	EM22_HUMAN	EM22_HUMAN
14	407	100.0	100	EM22_HUMAN	EM22_HUMAN
15	407	100.0	100	EM22_HUMAN	EM22_HUMAN
16	407	100.0	100	EM22_HUMAN	EM22_HUMAN
17	407	100.0	100	EM22_HUMAN	EM22_HUMAN
18	407	100.0	100	EM22_HUMAN	EM22_HUMAN
19	407	100.0	100	EM22_HUMAN	EM22_HUMAN
20	407	100.0	100	EM22_HUMAN	EM22_HUMAN
21	407	100.0	100	EM22_HUMAN	EM22_HUMAN
22	407	100.0	100	EM22_HUMAN	EM22_HUMAN
23	407	100.0	100	EM22_HUMAN	EM22_HUMAN
24	407	100.0	100	EM22_HUMAN	EM22_HUMAN
25	407	100.0	100	EM22_HUMAN	EM22_HUMAN
26	407	100.0	100	EM22_HUMAN	EM22_HUMAN
27	407	100.0	100	EM22_HUMAN	EM22_HUMAN
28	407	100.0	100	EM22_HUMAN	EM22_HUMAN
29	407	100.0	100	EM22_HUMAN	EM22_HUMAN
30	407	100.0	100	EM22_HUMAN	EM22_HUMAN
31	407	100.0	100	EM22_HUMAN	EM22_HUMAN
32	407	100.0	100	EM22_HUMAN	EM22_HUMAN
33	407	100.0	100	EM22_HUMAN	EM22_HUMAN

34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56	1.56


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Matches      17  Unannotated      0  Mismatches      0  Indels      0  Gaps
C2           246  STFAAF 132
              |||||
Dt           179  GFAAF 185

RESULT 30
FIND PYRAE
ID      PRAO PYRAE      STANDARD;      PRT;      345 AA.
AC      22115;
PT      15-JUN-2002 (rel. 41) (2003-03)
PT      16-JUN-2002 (rel. 41) (last sequence update)
PT      16-JUN-2002 (rel. 41) (last annotation update)
DE      Acidic ribosomal protein P0 homolog (L140F).
GN      RPLP0 OR PAB3107.
OS      Pyrobaculum aerophilum.

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[illegible]

[illegible][illegible]

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RESULT 60
DBH_GUTH          STANDARD      FFT      93 AA
AC    P20214,          STANDARD      FFT      93 AA
DT    01-DEC-1992 (Rel. 24, Created)
DI    01-DEC-1992 (Rel. 24, Last sequence update)
DI    16-OCT-2001 (Rel. 40, Last annotation update)
DE    DNA-binding protein H1 binding (Histone-like protein).
GN    H1P or H1PA Or H1P Or HPFC
OS    Galliardia theta (Cryptomonas ph.).
OG    Chloroplast.
OX    Eukaryota, Cryptophyta, Cryptisthaphanozoa, Galliardia.
RN    [NCBI_TaxId=55529;]
RP    SEQUENCE FROM N.A.
RX    MEDLINE:82073372, PubMed:1661745;
RA    Wang S., Liu X.-Q.;
RT    "The plastid genome of the cryptophyte alga, Galliardia theta
RT    contains a histone-like protein, and an additional protein".
PL    Proc Natl Acad Sci U S A 98:10902-10906(2001)
PI    [J.]
PP    SEQUENCE FROM N.A.
PX    MEDLINE:9419221, PubMed:9500000;
PY    Douglas S.E., Penny S.L.;
PT    "The plastid genome of the cryptophyte alga, Galliardia theta
PT    contains a histone-like protein, and an additional protein".
RL    J Mol Evol. 48:236-244(1999)
RI    [J.]
RJ    Protein. This protein belongs to the histone like family of
RJ    PROTEIN/DNA-BINDING PROTEINS WITH ARE CAPABLE OF BINDING
RJ    DNA TO STABILIZE IT, AND PREVENT ITS DEGRADATION UNDER EXTREME
RJ    ENVIRONMENTAL CONDITIONS (AT SIMILARITY
RJ    SIMILARITY PERCENTAGE TO THE BACTERIAL HISTONE H1 IS 10.0% EXACTLY).
CC    -----
CC    This SWISS-PROT entry is derived from a publication by Douglas et al. (1999), which states that the histone-like protein of Galliardia theta is a member of the histone-like protein family, and that it is involved in DNA packaging and chromatin organization. The authors also mention that the protein is highly conserved among different species of the genus Galliardia.
CC    between the Swiss Institute of Bioinformatics and the EMBL database.
CC    The European Bioinformatics Institute (EBI) has been notified and its consent is being sought as its name is used in the title of the entry.
CC    modified and this statement is not part of the entry. It will be removed if the author does not respond.
CC    entities requires a license agreement. See http://www.ebi.ac.uk/submit/
CC    or send an email to license@ebi.ac.uk.
CC    -----
CF    EMBL: AF041469; AAC02701;
CF    PIR: B41609; B41609;
CF    HSPD: P36206; 1987;
CF    InterPro: IPR00110, Eac DNABind;
CF    Pfam: PF00216, Bac DNA Binding;
CF    ProDom: PD000945, Bac_DNABind_1;
CF    SMART: SMO0411; BHL1;
CF    PROSITE: PS00045; HISTONE_LIKE_1
CF    DNA-binding DNA condensation; Chromoplast.
SV    SEQUENCE 93 AA; 1062 MW; 1EFAA0B0F0F45 DPO64.
Query March 1, 4%, Score 6, DB 1, Length 93
Best local similarity: 100.0%, Pied Mar 1, 2, 100
Matches 6; Conservation of Mismatches of Identity 0, Gap 0
Q# 355 ERYAPE 351
DA 54 ERYAPE 59
RESULT 61
DBH_ANASP         STANDARD      FFT      94 AA
AC    P05514; O57356;          STANDARD      FFT      94 AA
DI    01-NOV-1988 (Rel. 09, Created)
DI    01-NOV-1997 (Rel. 35, Last sequence update)
DI    15-JUN-2002 (Rel. 41, Last annotation update)
DE    DNA-binding protein HU.
GN    HUP OR HANA Or ASR345;

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01 Anabaena sp. (strain PCC 7120).
02 Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
03 NCBI_TaxId=103690;
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GenCore version 5.1.6
Copyright (c) 1994 - 2003 GenCore Inc.

OM Protein - Protein search, using sw method

Run on: Jun 30, 2003, 14:14:43, Path: /usr/local/GenCore
Without alignment: 2261235 Million cell updated/Sec

Title: US-09-905-744B-6
Perfect score: 428
Sequence: 1 MATWSTWTFWMTWVQVQVQV
ETWKAATATWTHLQVQVTH 419

Scoring table: OLIGO
Gap: 60.0, Gap: 60.0

Search: 671500 seqs, 2064715 residues

Word size: 0

Total number of hits satisfying chosen parameters: 671500

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 100 summaries

Database:

1: SP_archaea:
2: SP_bacteria:
3: SP_fungi:
4: SP_human:
5: SP_invertebrate:
6: SP_mammal:
7: SP_mhc:
8: SP_organelle:
9: SP_phage:
10: SP_plant:
11: SP_protist:
12: SP_virus:
13: SP_vertebrate:
14: SP_unclassified:
15: SP_virus:
16: SP_bacteriophage:
17: SP_archaeal:

Prod No is the number of results produced by choice. Have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match Length	DB	Prod No	Description
1	400	93.5	407	4	06XK15	Q6XK15 Homo sapien
2	395	93.2	407	4	06XK16	Q6XK16 Homo sapien
3	395	93.2	407	4	06XK17	Q6XK17 Homo sapien
4	395	93.2	407	4	06XK18	Q6XK18 Homo sapien
5	395	93.2	407	4	06XK19	Q6XK19 Homo sapien
6	395	93.2	407	4	06XK20	Q6XK20 Homo sapien
7	395	93.2	407	4	06XK21	Q6XK21 Homo sapien
8	395	93.2	407	4	06XK22	Q6XK22 Homo sapien
9	395	93.2	407	4	06XK23	Q6XK23 Homo sapien
10	395	93.2	407	4	06XK24	Q6XK24 Homo sapien
11	395	93.2	407	4	06XK25	Q6XK25 Homo sapien
12	395	93.2	407	4	06XK26	Q6XK26 Homo sapien
13	395	93.2	407	4	06XK27	Q6XK27 Homo sapien
14	395	93.2	407	4	06XK28	Q6XK28 Homo sapien
15	395	93.2	407	4	06XK29	Q6XK29 Homo sapien
16	395	93.2	407	4	06XK30	Q6XK30 Homo sapien

17	395	93.2	407	4	06XK31	Q6XK31 Homo sapien
18	395	93.2	407	4	06XK32	Q6XK32 Homo sapien
19	395	93.2	407	4	06XK33	Q6XK33 Homo sapien
20	395	93.2	407	4	06XK34	Q6XK34 Homo sapien
21	395	93.2	407	4	06XK35	Q6XK35 Homo sapien
22	395	93.2	407	4	06XK36	Q6XK36 Homo sapien
23	395	93.2	407	4	06XK37	Q6XK37 Homo sapien
24	395	93.2	407	4	06XK38	Q6XK38 Homo sapien
25	395	93.2	407	4	06XK39	Q6XK39 Homo sapien
26	395	93.2	407	4	06XK40	Q6XK40 Homo sapien
27	395	93.2	407	4	06XK41	Q6XK41 Homo sapien
28	395	93.2	407	4	06XK42	Q6XK42 Homo sapien
29	395	93.2	407	4	06XK43	Q6XK43 Homo sapien
30	395	93.2	407	4	06XK44	Q6XK44 Homo sapien
31	395	93.2	407	4	06XK45	Q6XK45 Homo sapien
32	395	93.2	407	4	06XK46	Q6XK46 Homo sapien
33	395	93.2	407	4	06XK47	Q6XK47 Homo sapien
34	395	93.2	407	4	06XK48	Q6XK48 Homo sapien
35	395	93.2	407	4	06XK49	Q6XK49 Homo sapien
36	395	93.2	407	4	06XK50	Q6XK50 Homo sapien
37	395	93.2	407	4	06XK51	Q6XK51 Homo sapien
38	395	93.2	407	4	06XK52	Q6XK52 Homo sapien
39	395	93.2	407	4	06XK53	Q6XK53 Homo sapien
40	395	93.2	407	4	06XK54	Q6XK54 Homo sapien
41	395	93.2	407	4	06XK55	Q6XK55 Homo sapien
42	395	93.2	407	4	06XK56	Q6XK56 Homo sapien
43	395	93.2	407	4	06XK57	Q6XK57 Homo sapien
44	395	93.2	407	4	06XK58	Q6XK58 Homo sapien
45	395	93.2	407	4	06XK59	Q6XK59 Homo sapien
46	395	93.2	407	4	06XK60	Q6XK60 Homo sapien
47	395	93.2	407	4	06XK61	Q6XK61 Homo sapien
48	395	93.2	407	4	06XK62	Q6XK62 Homo sapien
49	395	93.2	407	4	06XK63	Q6XK63 Homo sapien
50	395	93.2	407	4	06XK64	Q6XK64 Homo sapien
51	395	93.2	407	4	06XK65	Q6XK65 Homo sapien
52	395	93.2	407	4	06XK66	Q6XK66 Homo sapien
53	395	93.2	407	4	06XK67	Q6XK67 Homo sapien
54	395	93.2	407	4	06XK68	Q6XK68 Homo sapien
55	395	93.2	407	4	06XK69	Q6XK69 Homo sapien
56	395	93.2	407	4	06XK70	Q6XK70 Homo sapien
57	395	93.2	407	4	06XK71	Q6XK71 Homo sapien
58	395	93.2	407	4	06XK72	Q6XK72 Homo sapien
59	395	93.2	407	4	06XK73	Q6XK73 Homo sapien
60	395	93.2	407	4	06XK74	Q6XK74 Homo sapien
61	395	93.2	407	4	06XK75	Q6XK75 Homo sapien
62	395	93.2	407	4	06XK76	Q6XK76 Homo sapien
63	395	93.2	407	4	06XK77	Q6XK77 Homo sapien
64	395	93.2	407	4	06XK78	Q6XK78 Homo sapien
65	395	93.2	407	4	06XK79	Q6XK79 Homo sapien
66	395	93.2	407	4	06XK80	Q6XK80 Homo sapien
67	395	93.2	407	4	06XK81	Q6XK81 Homo sapien
68	395	93.2	407	4	06XK82	Q6XK82 Homo sapien
69	395	93.2	407	4	06XK83	Q6XK83 Homo sapien
70	395	93.2	407	4	06XK84	Q6XK84 Homo sapien
71	395	93.2	407	4	06XK85	Q6XK85 Homo sapien
72	395	93.2	407	4	06XK86	Q6XK86 Homo sapien
73	395	93.2	407	4	06XK87	Q6XK87 Homo sapien
74	395	93.2	407	4	06XK88	Q6XK88 Homo sapien
75	395	93.2	407	4	06XK89	Q6XK89 Homo sapien
76	395	93.2	407	4	06XK90	Q6XK90 Homo sapien
77	395	93.2	407	4	06XK91	Q6XK91 Homo sapien
78	395	93.2	407	4	06XK92	Q6XK92 Homo sapien
79	395	93.2	407	4	06XK93	Q6XK93 Homo sapien
80	395	93.2	407	4	06XK94	Q6XK94 Homo sapien
81	395	93.2	407	4	06XK95	Q6XK95 Homo sapien
82	395	93.2	407	4	06XK96	Q6XK96 Homo sapien
83	395	93.2	407	4	06XK97	Q6XK97 Homo sapien
84	395	93.2	407	4	06XK98	Q6XK98 Homo sapien
85	395	93.2	407	4	06XK99	Q6XK99 Homo sapien
86	395	93.2	407	4	06XK100	Q6XK100 Homo sapien
87	395	93.2	407	4	06XK101	Q6XK101 Homo sapien
88	395	93.2	407	4	06XK102	Q6XK102 Homo sapien
89	395	93.2	407	4	06XK103	Q6XK103 Homo sapien
90	395	93.2	407	4	06XK104	Q6XK104 Homo sapien
91	395	93.2	407	4	06XK105	Q6XK105 Homo sapien
92	395	93.2	407	4	06XK106	Q6XK106 Homo sapien
93	395	93.2	407	4	06XK107	Q6XK107 Homo sapien
94	395	93.2	407	4	06XK108	Q6XK108 Homo sapien
95	395	93.2	407	4	06XK109	Q6XK109 Homo sapien
96	395	93.2	407	4	06XK110	Q6XK110 Homo sapien
97	395	93.2	407	4	06XK111	Q6XK111 Homo sapien
98	395	93.2	407	4	06XK112	Q6XK112 Homo sapien
99	395	93.2	407	4	06XK113	Q6XK113 Homo sapien
100	395	93.2	407	4	06XK114	Q6XK114 Homo sapien

1. *Phragmites australis* (Cav.) Trin. ex Steud.

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DR EMBL: AB027635, BAB02211, 100% Identity, 100% Coverage, 100% Length, 100% Score, 100% Positives, 100% Negatives, 100% Matches, 100% Conserved, 100% Mismatches, 100% Indels, 100% Gaps

Query Match 1.98, Score 8, DB 10, Length 407,
Best Local Similarity 100.0%, Pred. No. 20,
Matches 8, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 129 ATAGIRL 136
DB 76 ATAGIRL 83

RESULT 17

QY EMBL: AB027635, BAB02211, 100% Identity, 100% Coverage, 100% Length, 100% Score, 100% Positives, 100% Negatives, 100% Matches, 100% Conserved, 100% Mismatches, 100% Indels, 100% Gaps

Query Match 1.98, Score 8, DB 10, Length 407,
Best Local Similarity 100.0%, Pred. No. 20,
Matches 8, Conservative 0, Mismatches 0, Indels 0, Gaps 0

RESULT 18

QY EMBL: AB027635, BAB02211, 100% Identity, 100% Coverage, 100% Length, 100% Score, 100% Positives, 100% Negatives, 100% Matches, 100% Conserved, 100% Mismatches, 100% Indels, 100% Gaps

QY EMBL: AB027635, BAB02211, 100% Identity, 100% Coverage, 100% Length, 100% Score, 100% Positives, 100% Negatives, 100% Matches, 100% Conserved, 100% Mismatches, 100% Indels, 100% Gaps

DR EMBL: AB027635, BAB02211, 100% Identity, 100% Coverage, 100% Length, 100% Score, 100% Positives, 100% Negatives, 100% Matches, 100% Conserved, 100% Mismatches, 100% Indels, 100% Gaps

Query Match 1.98, Score 8, DB 10, Length 407,
Best Local Similarity 100.0%, Pred. No. 20,
Matches 8, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 43 VSASTLYG 50
DB 106 VSASTLYG 113

RESULT 19

QY EMBL: AB027635, BAB02211, 100% Identity, 100% Coverage, 100% Length, 100% Score, 100% Positives, 100% Negatives, 100% Matches, 100% Conserved, 100% Mismatches, 100% Indels, 100% Gaps

Query Match 1.98, Score 8, DB 10, Length 407,
Best Local Similarity 100.0%, Pred. No. 20,
Matches 8, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 129 ATAGIRL 136
DB 76 ATAGIRL 83

RESULT 20

QY EMBL: AB027635, BAB02211, 100% Identity, 100% Coverage, 100% Length, 100% Score, 100% Positives, 100% Negatives, 100% Matches, 100% Conserved, 100% Mismatches, 100% Indels, 100% Gaps

QY EMBL: AB027635, BAB02211, 100% Identity, 100% Coverage, 100% Length, 100% Score, 100% Positives, 100% Negatives, 100% Matches, 100% Conserved, 100% Mismatches, 100% Indels, 100% Gaps

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DT 01-NOV-1998 (TREMUR) 08, Last sequence update)
 DT 01-DEC-2001 (TREMUR) 19, Last annotation update)
 DE GP120 (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1
 CC Viruses; Retroviral viruses; Lentiviridae; Lentivirus
 CC NCBI_TaxID:11676;
 RN (1)
 PP SEQUENCE FROM N.A.
 RC STRAIN=96CH17;
 RX MEDLINE 2914662, PubMed:10024057,
 RA Chen T, Young N L, Subbarao S, Marichev P, Sagnunwongse S,
 PA McCosker S, Jayaram C, Luo C C, Mastror T D 1996,"
 RT HIV type 1 subtypes in Guangxi Province, China, 1996,"
 RI AIDS Res Hum Retroviruses 15:81-84(1999)
 DR FMRU, AF090312, AF090412;
 DP InterPro: IPR000777, GP120
 DE Pfam, PF00516, GP120,
 FW Pfam, Pfam:00516, GP120
 FT NON-TER 1
 FT NON-TER 1
 ST SEQUENCE 115 AA, 1150 MW, 212674.47 kDa (PF004)

Query Match 1.68; Score 7; DB 15; Length 115;
 Best Local Similarity 100.0%; Pos: 11; 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 EXTEND 220
 DB 63 EXTEND 69

RESULT 19
 09:520
 ID 09F820 FREEDMINARY, ENT, 123 AA.
 AC 09F820;
 DT 01-MAR-2001 (TREMUR) 16, Created)
 DT 01-MAR-2001 (TREMUR) 16, Last sequence update)
 DT 01-JUN-2002 (TREMUR) 01, Last annotation update)
 DE Apyrase (Fragment)
 OS Pisum sativum (Garden pea)
 CC Eukaryota; Eukaryota; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons; Euasteridae;
 CC Eusteroideae; Fabales; Fabaceae; Papilionales; Viciales; Pisum
 CC NCBI_TaxID=3888;
 RN (1)
 PP SEQUENCE FROM N.A.
 RC STRAIN=ALASKA; TISSE-DARY GROWN STEM INTERNOE;
 RA Yoneda M, Shibata K, Abe S;
 RI Submitted (JUL-1999) to the EMBL/GenBank/CCDB databases;
 RN (2)
 PP SEQUENCE FROM N.A.
 RC STRAIN=ALASKA; TISSE-DARY GROWN STEM INTERNOE;
 RA Shibata K, Abe S, Davies E;
 RT "Structure of the coding region and mRNA variants of the *apyrase* gene"
 RT Pisum sativum";
 RI Acta Physiol Plant 20:313(2001)
 DR FMRU, AB010444; BAB09011;
 DP InterPro: IPR000407, GDAI_CDAI_INTERNOE;
 DR Pfam: PF01150, GDAI_CDAI_1
 FT NON-TER 123
 FT NON-TER 123
 ST SEQUENCE 123 AA, 12710 MW, 50441.091 kDa (PF004)

Query Match 1.68; Score 7; DB 15; Length 115;
 Best Local Similarity 100.0%; Pos: 11; 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 FDAGSTG 59
 DB 48 FDAGSTG 54

RESULT 40

Q91E44
 ID Q91E44 FREEDMINARY, ENT, 133 AA.
 AC Q91E44;
 DT 01-OCT-2000 (TREMUR) 15, Created;
 DT 01-OCT-2000 (TREMUR) 15, Last sequence update)
 DE 01-DEC-2001 (TREMUR) 19, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 CC Viruses; Retroviral viruses; Lentiviridae; Lentivirus.
 CC NCBI_TaxID=11676;
 RN (1)
 PP SEQUENCE FROM N.A.
 RC STRAIN=96CH17;
 RA Ruyter P, Peterson D, Demont E, Sussknecht G, Mauchle P,
 PA Peterson D, Peterson D, Peterson D, Peterson P,
 RT "Envelope glycoprotein analysis and putative HIV-1 isolates,"
 RI Submitted (JUL-1999) to the EMBL/GenBank/CCDB databases;
 DE EMBL, AF090312, AF090412;
 DP InterPro: IPR000777, GP120.
 DE Pfam, PF00516, GP120, 1.
 FW Pfam, Pfam:00516, GP120, 1.
 FT NON-TER 1
 FT NON-TER 1
 ST SEQUENCE 133 AA, 1330 MW, 19740.191 kDa (PF004)

Query Match 1.68; Score 7; DB 15; Length 133;
 Best Local Similarity 100.0%; Pos: 10; 76;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 214 EXTEND 220
 DB 111 EXTEND 117

RESULT 41
 09:540
 ID 09E400 FREEDMINARY, ENT, 124 AA.
 AC 09E400;
 DT 01-AUG-1998 (TREMUR) 07, Created)
 DT 01-AUG-1998 (TREMUR) 07, Last sequence update)
 DT 01-MAR-2002 (TREMUR) 02, Last annotation update)
 DE Hypothetical protein F00770.
 RN (1)
 PP Pyrococcus horikoshii.
 OS Pyrococcus horikoshii.
 CC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
 CC Pyrococcus.
 CC NCBI_TaxID=59283;
 RN (1)
 PP SEQUENCE FROM N.A.
 RC STRAIN=073;
 RX MEDLINE 2914662, PubMed:10024057;
 RA Kawabuchi Y, Shimada M, Horiuchi H, Horiuchi Y, Horiuchi Y,
 PA Yamamoto S, Sekine M, Sakai T, Horiuchi H, Horiuchi A, Horiuchi Y,
 PA Kikuchi Y, Otsuka T, Otsuka T, Horiuchi H, Horiuchi A, Horiuchi Y,
 PA Horiuchi T, Tanaka T, Kudo Y, Yamazaki T, Kudo N, Otsuka A,
 RA Horiuchi Y, Horiuchi T, Horiuchi A, Horiuchi Y, Horiuchi A,
 RA Masuda Y, Shimada M, Horiuchi H;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii 073,"
 RI DNA Res 5:55-76(1998).
 DR EMBL, AF090312, AF090412;
 DP InterPro: IPR001993, Mitochondrial carrier.
 DE EMBL, AF090312, AF090412;
 FW Hypothetical protein F00770.
 ST SEQUENCE 124 AA, 12400 MW, 19740.191 kDa (PF004)

Query Match 1.68; Score 7; DB 17; Length 154;
 Best Local Similarity 100.0%; Pos: 11; 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 LUGSLGT 426

[illegible]

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Query Word(s) : 100.0%   E-Value = 0.00E+00
Best Local Similarity: 100.0%; Posed No.: 95;
Matches      7; Conservative    0; Mismatches     0; Indels       0; Gaps          0

Cy             368 STVOLT 472
                |||||
Db            35 STVOLT 41

RESULT 46
C05333         PRELIMINARY;           FRT);    185 AA.
ID C05333
AC C05333;
DT 01-JUL-1997 (TRENKLE) 04, Created)
DT 01-JUL-1997 (TRENKLE) 04, Last sequence update)
DI 01-MAR-2003 (TRENKLE) 20, last annotation update)
DE Fort ATP synthase, stromal P
GN ATPF.
OS Phosphatoyl transferase [Phosphotransferase system]
OC Bacteria, Proteobacteria, alpha Subdivision, Rhodospirillum rubrum group;
CC Rhodobacter
OX NCBI_Taxid:1061.
PY 111
PE SEQUENCE FROM N.A.
PX MEDLINE=99035763; PubMed=9818357;
RA Boeghsche R., Turina P., Lambertini L., Melandri P A /
RT "The atPFX gene coding for the P-subunit of the ATP synthase from Rhodospirillum rubrum encodes a phosphotransferase".
PT Capsulation ".
PL Arch Microbiol 170 (1997) 661-668)
DB EMBL; Y1011; CAB00904 .

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[illegible][illegible]

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SN      11)
PT      SOURCE FROM N.A.
PA      Wallis J.M.
PR      Submitted (1984-1985) to the EMBL/Gen Bank/CCDB database.
PN      12)
PP      SOURCE FROM N.A.
PX      KENNEDY, GORDON, FORD 1981:6.
PY      none.
PT      "Genetic structure of the American white sturgeon, Acipenser transmontanus (Richardson)"
PA      Science 223: 603-604 (1984).
PR      EMBL, Accession: EMB0383.1.
PN      13)
PP      "Genetic structure of the American white sturgeon, Acipenser transmontanus (Richardson)"
PX      FORD, GORDON, KENNEDY 1981:1.
PY      none.
PT      SMART, SMOORE, FORD 1981.
PR      POSITIVE (SODAP, EXON) 1.
PN      14)
PP      "Genetic structure of the American white sturgeon, Acipenser transmontanus (Richardson)"
PX      FORD, GORDON, KENNEDY 1981:6.
PY      none.

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GenCore version 5.1.6
CSeqY31317.1.1991.2003 CSeqY31317.1

OM protein - protein search, using SW 00341

Run on 3/20/2003, 14:51:42, Search: 11/23/2003

(without alignment)
1462,340 Million cell updates/sec

Title:

US-09-905-744b-6

Perfect score:

428

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Sequence:

01190

Gap: 60 0, Gap: 60 0

Scoring: 1110

Gap: 60 0, Gap: 60 0

Searched:

40470 seqs, 111050620 residues

Word size:

0

Total number of hits satisfying chosen parameters: 20470

Minimum E:

1.1e-11

Maximum DP:

200000000

Post-processing:

Listing first 100 summaries

Database:

A Geneset 101002

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	428	100.0	428	21	AAV44844
4	428	100.0	428	21	AAV44844
5	400	99.5	400	21	AAV44844
6	400	99.5	400	21	AAV44844
7	400	99.5	400	21	AAV44844
8	400	99.5	400	21	AAV44844
9	400	99.5	400	21	AAV44844
10	400	99.5	400	21	AAV44844

11	58	13.6	58	21	AAV70326	Human CD39-14 FRO
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13	46	10.7	46	22	ABD13553	Human protein #71
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100	46	10.7	46	22	AAV70326	Human protein #71

XX Example 4: SEQ ID NO: 26150; 650bp + Sequence Listing, English.
 PS The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences of breast and human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention.

SO Sequence 46 AA;

Query Match 10.7% Score 46; DB 22; Length 46;
 Best Local Similarity 100.0%; Seed No. 170-29;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0

297 EWGFFCYAVFVPTVPTTHOFFEYQSTSFATWYQPAVDYDVI 342
 1 FVGFECYAEVLPVPSFLHPSEVPSSTFASSTYDPAVDYDVI 46

RESULT 16
 ID AAM6436 standard; Protein; 46 AA.
 AC AAM6436.
 XX 06-NOV-2001 (first entry)
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26740
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26740
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26740
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26740
 XX Human bone marrow expressed probe encoded protein SEQ ID NO: 26740
 XX Homo sapiens.
 XX W0200157276 AD.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US 0190312.
 XX 26-MAY-2000; 2000US 0207456.
 XX 30-JUN-2000; 2000US 0209409.
 XX 03-AUG-2000; 2000US 0213165.
 XX 21-SEP-2000; 2000US 0214687.
 XX 27-SEP-2000; 2000US 0216152.
 XX 04-OCT-2000; 2000US 0214769.
 XX (MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI: 2001 489901/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow.
 XX Example 4: SEQ ID NO: 26740; 658bp + Sequence Listing, English.
 PS The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in bone marrow
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of
 CC such as lymphoma, leukemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention.

SO Sequence 46 AA;

Query Match 10.7% Score 46; DB 22; Length 46;
 Best Local Similarity 100.0%; Seed No. 170-29;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0

297 EWGFFCYAVFVPTVPTTHOFFEYQSTSFATWYQPAVDYDVI 342
 1 FVGFECYAEVLPVPSFLHPSEVPSSTFASSTYDPAVDYDVI 46

RESULT 17
 ID AAM14306 standard; Protein; 46 AA.
 AC AAM14306.
 XX 10-OCT-2001 (first entry)
 DE Cervical cancer.
 XX Cervical cancer.
 XX Cervical cancer.
 XX Cervical cancer.
 XX Cervical cancer.
 XX Homo sapiens.
 XX W0200157276 AD.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US 0190312.
 XX 26-MAY-2000; 2000US 0207456.
 XX 30-JUN-2000; 2000US 0209409.
 XX 03-AUG-2000; 2000US 0213165.
 XX 21-SEP-2000; 2000US 0214687.
 XX 27-SEP-2000; 2000US 0216152.
 XX 04-OCT-2000; 2000US 0214769.
 XX (MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI: 2001 489901/53.
 XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human cervical epithelial cells.
 XX Example 4: SEQ ID NO: 26740; 658bp + Sequence Listing, English.

XX The present invention relates to human single exon nucleic acid probes
 CC which are derived from genomic sequences expressed in a peptide encoded
 CC by the single probe. The probes are derived from human cells. The probes
 CC can be used to measure gene expression in a sample derived from human
 CC cervical cells. By measuring gene expression, the probes are therefore
 CC useful in diagnosing and treating diseases of the cervix, notably
 CC cervical cancer.
 CC The present sequence data for this patent did not form part of the present
 CC specification, but was obtained in accordance with the requirements of the
 CC WIPO Patent Treaty.

SO Sequence 46 AA;

Query Match 10.7% Score 46; DB 22; Length 46;
 Best Local Similarity 100.0%; Seed No. 170-29;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0

297 EWGFFCYAVFVPTVPTTHOFFEYQSTSFATWYQPAVDYDVI 342
 1 FVGFECYAEVLPVPSFLHPSEVPSSTFASSTYDPAVDYDVI 46

RESULT 18
 ID AAM26716 standard; Protein; 46 AA.
 AC AAM26716.
 XX 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US00668.

XX (IMMUNEX CORP)
 PA Maltsevskii CR, Gayle EB, Fricke W, Grapel CD,
 XX WP1: 2000-339518/23
 XX
 PT New soluble CD39 polypeptides having activity in inhibiting platelet aggregation and preventing unstable angina, myocardial infarction, stroke, coronary artery disease or injury -
 PT Claim 6: Page 91-93; 120FF; English
 XX
 CC The present sequence is a fusion protein construct (CD39-14-23)
 CC comprising the human CD39-L4 N-terminal region and soluble CD39
 CC CD39-L4 is a secreted glycoprotein belonging to the CD39 family. Soluble CD39
 CC is characterized by removal of N- and C-terminal transmembrane domains. It
 CC retains the capacity to metabolize ADP and ADP at relevant concentrations
 CC and the ability to block and reverse ADP induced platelet activation and
 CC recruitment, including platelet aggregation. Soluble CD39 polypeptides
 CC are useful for inhibiting angiogenesis. It is useful for the treatment
 CC of unstable angina, myocardial infarction, stroke, coronary artery
 CC disease or injury, thrombotic events, peripheral vascular disease, including
 CC peripheral artery disease, platelet associated ischemic disorders including
 CC lung, coronary and cerebral ischemia, thrombotic disorders including
 CC coronary, peripheral and cerebral artery thrombosis, pulmonary and
 CC venous thrombosis, coagulopathy, deep venous thrombosis (DVT), stroke,
 CC embolism (PE) and transient ischemic attack (TIA). Soluble CD39 is also
 CC useful for preventing thrombus formation in atherothrombotic conditions,
 CC recanalization, stenosis or restenosis of blood vessels or stroke.
 CC
 CC Sequence 476 AA:
 XX
 XX Query Match 9.6% Score 39, E-03, Length 476,
 XX Best Local Similarity 100.0%, From No. 1 seq. 10
 XX Matches 38; Conservation 0; Mismatches 0; Indels 0; gaps 0
 XX
 XX 1 MATSWTFVFMVLTGVSNAVSHPRQVWVWVFLQSM 38
 XX 1 MATSWTFVFMVLTGVSNAVSHPRQVWVWVFLQSM 38
 XX
 XX RESULT 24
 XX AA70888 standard, protein: 476 AA.
 XX
 XX AC AA70888:
 XX
 XX 17-AUG-2000 (first entry)
 XX
 XX Protein encoded by CD39-L4-1 construct.
 XX
 XX Soluble CD39, human glycoprotein activity; platelet activation; inhibition;
 XX unstable angina, myocardial infarction, stroke, coronary artery disease,
 XX thrombotic events, peripheral vascular disease, including lung, coronary
 XX platelet associated ischemic disorders, thrombotic disorders including
 XX cerebral ischemia, thrombotic disorders including pulmonary and
 XX cerebral artery thrombosis, coagulopathy, deep venous thrombosis (DVT),
 XX peripheral artery thrombosis, coagulopathy, deep venous thrombosis (DVT),
 XX stroke, embolism (PE) and transient ischemic attack (TIA). Soluble CD39
 XX is also useful for preventing thrombus formation in atherothrombotic
 XX conditions, stenosis or restenosis of blood vessels or stroke.
 XX
 XX Homologous: human glycoprotein activity; platelet activation; inhibition;
 XX Synthesis:
 XX
 XX Key Location/Qualifications
 XX Cleavage-site 20-21
 XX Region 1-37
 XX /notes "Derived from CD39-L4"
 XX /dones "soluble portion of CD39"

XX
 XX Maltsevskii CR, Gayle EB, Fricke W, Grapel CD,
 XX WP1: 2000-339518/23
 XX
 PT Inhibiting platelet activation and recruitment; useful for treatment of
 PT unstable angina, myocardial infarction, stroke, coronary artery disease or
 PT injury, thrombotic events, peripheral vascular disease, including lung,
 PT coronary and cerebral artery thrombosis, pulmonary and venous thrombosis,
 PT coagulopathy, deep venous thrombosis (DVT), stroke, embolism (PE) and
 PT transient ischemic attack (TIA). Soluble CD39 is also useful for preventing
 PT thrombus formation in atherothrombotic conditions, stenosis or restenosis
 PT of blood vessels or stroke.
 PT
 PT Sequence 476 AA:
 XX
 XX Query Match 9.6% Score 37, E-03, Length 476,
 XX Best Local Similarity 100.0%, From No. 1 seq. 28
 XX Matches 37; Conservation 0; Mismatches 0; Indels 0; gaps 0
 XX
 XX 1 MATSWTFVFMVLTGVSNAVSHPRQVWVWVFLQSM 37
 XX 1 MATSWTFVFMVLTGVSNAVSHPRQVWVWVFLQSM 37
 XX
 XX RESULT 25
 XX AA70911
 XX
 XX 17-AUG-2000 (first entry)
 XX
 XX Protein encoded by CD39-L4-1 construct.
 XX
 XX Soluble CD39, human glycoprotein activity; platelet activation; inhibition;
 XX unstable angina, myocardial infarction, stroke, coronary artery disease,
 XX thrombotic events, peripheral vascular disease, including lung, coronary
 XX platelet associated ischemic disorders, thrombotic disorders including
 XX cerebral ischemia, thrombotic disorders including pulmonary and
 XX cerebral artery thrombosis, coagulopathy, deep venous thrombosis (DVT),
 XX peripheral artery thrombosis, coagulopathy, deep venous thrombosis (DVT),
 XX stroke, embolism (PE) and transient ischemic attack (TIA). Soluble CD39
 XX is also useful for preventing thrombus formation in atherothrombotic
 XX conditions, stenosis or restenosis of blood vessels or stroke.
 XX
 XX Homologous: human glycoprotein activity; platelet activation; inhibition;
 XX Synthesis:
 XX
 XX Key Location/Qualifications
 XX Cleavage-site 20-21
 XX Region 1-37
 XX /notes "Derived from CD39-L4"
 XX /dones "soluble portion of CD39"

KM Rheumatoid arthritis; ataxia; osteoporosis; arthritis-jarvis; j'artima;
 KM inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KM infectivity; Cardiovascular disease; coagulation disorder; hypertension;
 KM ischaemia; asthma; immune disease; epilepsy; angina; neurodegenerative
 KM diabetes; anxiety; depression; schizophrenia; viral disease stroke;
 KM gastric ulcer; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN W0200206315-A2.
 XX
 PD 24 JAN-2002.
 XX
 PE 17-JUL-2001, 2001W0206315-A2.
 XX
 PP 18-JUL-2000; 2000JL-017245.
 PP 15-DEC-2000; 2000JL-017054.
 XX
 PA (COMP-) COMPUGEN LTD.
 XX
 PI Mintz L, Freilich S, Bernstein J;
 XX
 DP WPI, 2002-155037/20.
 DP N-PSDB; ABU39779.
 XX
 PT One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing a/2 cancer, asthma and Alzheimer's.
 XX
 PS Claim 6, Page 251-261, 2000F, English.
 XX
 CC ABL39691 to ABL39699 represent novel human nucleic acid sequences
 CC encoding the proteins given in Appendix 1 to Appendix 14. The novel sequences
 CC (NS) can have cytostatic, osteoprotic, synaptogenic, neuroprotective,
 CC antithrombotic, antipathologic, antiparasitic, ophthalmologic, virologic,
 CC vasorelaxant, antiarthrosclerotic, antidiabetic, dermatologic, anti-
 CC anorectic, muscular, anti-HIV, antileukemic, antitumor, anti-
 CC antineoplastic, antihypertensive, hypotensive, antidiabetic, anti-
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilizer, anti-
 CC neurodegenerative, gastrointestinal, neuroleptic, neuroprotective,
 CC neurotropic and contraceptive activities. The NS can be used in vaccine,
 CC gene therapy and antisense therapy. Nucleic acids, expressed in vac-
 CC cine antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dyscrania, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC catarrhes, retinitis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infectivity, cardiovascular
 CC disease, coagulation disorder, ischaemia, hypertension, angina, immu-
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcer, stroke,
 CC Alzheimer's disease and as a contraceptive.
 XX
 SQ Sequence 463 AA;
 XX
 QY Query Match 3.0%, Score 13, PR 22, Length 471,
 Db Best Local Similarity 100.0%, Prod No. 0.00033,
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 RESULT 32
 AAB72242
 ID AAB72242 standard, Protein, 471 AA.
 XX
 AC AAB72242;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Mature human CD19 like protein CD19 is a trans acid sequence.
 XX
 FE Human CD19 like protein; deyrase, NCPase, platelet function inhibitor,

PW myocardial infarction, cerebral thrombosis, angina; arterial thrombosis;
 PW cerebral artery thrombosis; stroke; aggragation; inflammation;
 PW agglutination; immune disorder; neurological disorder;
 PW Alzheimer's disease; Parkinson's disease; cancer; AIDS; L2.
 XX
 OS Homo sapiens.
 XX
 PN W020010205-A1.
 XX
 PD 15-FEB-2001.
 XX
 PE 02-APR-2000; 2000W02051790.
 XX
 PP 11-JAN-2000; 2000ms 0481284.
 PP 07-APR 2000; 2000ms 0507900.
 PP 16-MAY-2000; 2000ms 0502231.
 PP 10-JUN-2000; 2000ms 0600285.
 XX
 PA (HSE-) HSECO INC.
 XX
 PI Ford J, Mulero JJ, Yeung G;
 XX
 DP WPI, 2001-147437/15.
 DP N-PSDB; AAF63187.
 XX
 PT Polypeptides encoding human CD19 like polypeptides with affase
 PT and/or NDase activity, which are useful in the treatment of
 PT various viral infections, including AIDS, and J'artima;
 PT infection) and inflammatory disorders.
 XX
 PS Claim 23, Page 120-124, 2000F, English.
 XX
 CC This invention relates to polypeptides encoding human CD19 like
 CC polypeptides with affase and/or NDase activity. Polypeptides having
 CC affase, including NDase, activity are useful for inhibiting platelet
 CC function and can likewise be used in the prophylaxis or treatment of
 CC cardiovascular diseases caused by atherosclerosis or excessive
 CC coagulation or excessive platelet aggregation, such as myocardial
 CC infarction, cerebral ischemia, angina, arterial thrombosis, cerebral
 CC artery thrombosis or stroke. Polypeptides having NDase activity are
 CC useful for treating and/or preventing diseases associated
 CC with thrombocytosis, such as stroke, myocardial infarction, associated
 CC with metastatic disease states (including prostate aggregation), inflammation
 CC and aggragation, associated with HIV or other retroviral signaling by
 CC reducing the levels of CD19. The polypeptides are also useful for
 CC prophylaxis or treatment of infections related disorders, such as
 CC AIDS (and associated diseases), cytomegalovirus infection, malaria, L2,
 CC cytomegalovirus infection, autoimmune disorders such as rheumatoid
 CC arthritis, osteoporosis, stroke, Parkinson's disease, including psoriasis,
 CC catarrhes, retinitis, atherosclerosis, inflammation, skin disorders,
 CC neurological disorders including neurodegenerative diseases, epilepsy,
 CC depression, Alzheimer's disease, Parkinson's disease, Huntington's
 CC disease, and aggragation, including catarrhes, and cancer and present
 CC sequence represented mature CD19 like protein CD19-L2.
 XX
 SQ Sequence 471 AA;
 XX
 QY Query Match 3.0%, Score 13, DB 22, Length 471,
 Db Best Local Similarity 100.0%, Prod No. 0.00033,
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 RESULT 33
 AAB72241
 ID AAB72241 standard, Protein, 464 AA.
 XX
 AC AAB72241;
 XX

XX Drosophila, developmental biology, cell signalling, immunology,
 XX pharmaceutical.
 XX Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 27-MAR-2001; 2001WO-0500021.
 XX 23-MAR-2000; 2000US-14-47P.
 XX 11-JUL-2000; 2000US-04-47P.
 XX (PENE) FE CORF NT.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI, 2001 656660/75.
 XX N-PSDB; AB010316.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX Disclosure: SEQ ID NO 6431, 21P - Sequence listing: English.
 XX PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB010316-AB010317), expressed DNA
 CC sequences (AB010440-AB010475) and the encoded proteins
 CC (AAB07737-AAB07739).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wpi.int/pub/published_pcl_sequences.
 XX SO Sequence 461 AA;
 XX Query March 2001; Score 12; DB 22; Length 461;
 XX Fast Local similarity 100.0%, Prod N 2000;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 126 VKATAGRLRP 137
 XX |||||||
 XX DB 156 VKATAGRLRP 167
 XX
 XX RESULT 36
 XX ABB59611
 XX ID ABB59611 standard; Protein: 464 AA
 XX XX
 XX ABB59611;
 XX 27-MAR-2000 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 5625.
 XX XX
 XX Drosophila; developmental biology, cell signalling, immunology,
 XX pharmaceutical.
 XX Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-0500021.
 XX N-PSDB; AB010316.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX Disclosure: SEQ ID NO 6431, 21P - Sequence listing: English.
 XX PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB010316-AB010317), expressed DNA
 CC sequences (AB010440-AB010475) and the encoded proteins
 CC (AAB07737-AAB07739).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wpi.int/pub/published_pcl_sequences.
 XX SO Sequence 464 AA;
 XX Query March 2001; Score 12; DB 22; Length 461;
 XX Fast Local similarity 100.0%, Prod N 2000;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 126 VKATAGRLRP 137
 XX |||||||
 XX DB 156 VKATAGRLRP 167
 XX
 XX RESULT 37
 XX ABB19882
 XX ID ABB19882 standard; Protein: 464 AA
 XX XX
 XX ABB19882;
 XX 27-MAR-2000 (first entry)
 XX DE Human CD39L3 protein.
 XX XX
 XX Human; CD-39-like protein; CD39L3 protein; therapy; immune deficiency;
 KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
 KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
 KW osteoarthritis; wound healing; stroke; kidney; Alzheimer's disease; HIV;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 KW nervous system disease; nerve injury; ischemia reperfusion injury;
 KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
 KW Crohn's disease; vitreous detachment; aneurysm; neuroprotection;
 KW hemangioma; hemangioma; hemangioma; hemangioma; hemangioma;
 KW antiinflammatory; nephropathy; gastroenteritis; vasculopathy;
 XX XX
 XX Homo sapiens.
 XX US635C447-B1.
 XX 46-FEB-2002.
 XX 27-MAR-2001; 2001US-043739.
 XX 23-JAN-1999; 1999US-0240699.
 XX (HUSE) HUSEQ INC.
 XX CHADWICK EP, FRIEDBAUF A;

PR 11-JUL-2000; 2000US-061415C.
 XX (PENE) FE CORF NT.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI, 2001 656660/75.
 XX N-PSDB; AB010314.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX Disclosure: SEQ ID NO 6005, 21P - Sequence listing: English.
 XX PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB010316-AB010317), expressed DNA
 CC sequences (AB010440-AB010475) and the encoded proteins
 CC (AAB07737-AAB07739).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wpi.int/pub/published_pcl_sequences.
 XX SO Sequence 464 AA;
 XX Query March 2001; Score 12; DB 22; Length 461;
 XX Fast Local similarity 100.0%, Prod N 2000;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 126 VKATAGRLRP 137
 XX |||||||
 XX DB 156 VKATAGRLRP 167
 XX
 XX RESULT 37
 XX ABB19882
 XX ID ABB19882 standard; Protein: 464 AA
 XX XX
 XX ABB19882;
 XX 27-MAR-2000 (first entry)
 XX DE Human CD39L3 protein.
 XX XX
 XX Human; CD-39-like protein; CD39L3 protein; therapy; immune deficiency;
 KW autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
 KW rheumatoid arthritis; autoimmune thyroiditis; allergic reaction; asthma;
 KW insulin dependent diabetes mellitus; periodontal disease; osteoporosis;
 KW osteoarthritis; wound healing; stroke; kidney; Alzheimer's disease; HIV;
 KW Parkinson's disease; amyotrophic lateral sclerosis; Huntington's disease;
 KW nervous system disease; nerve injury; ischemia reperfusion injury;
 KW endotoxin lethality; arthritis; nephritis; inflammatory bowel disease;
 KW Crohn's disease; vitreous detachment; aneurysm; neuroprotection;
 KW hemangioma; hemangioma; hemangioma; hemangioma; hemangioma;
 KW antiinflammatory; nephropathy; gastroenteritis; vasculopathy;
 XX XX
 XX Homo sapiens.
 XX US635C447-B1.
 XX 46-FEB-2002.
 XX 27-MAR-2001; 2001US-043739.
 XX 23-JAN-1999; 1999US-0240699.
 XX (HUSE) HUSEQ INC.
 XX CHADWICK EP, FRIEDBAUF A;

21 Beadolin AP, Sengupta A;
XX
XX WPI: 1997-47702/47
XX
XX Isolated APL (Phosphi) high 1350 enzymes have and have a high
PT activity, useful for reducing platelet aggregation and
PT thrombogenicity
XX
XX Claim 3, Page 46, 60FF, English.
XX
XX The bovine atria (AAW01191 + AAW01192 and AAW01193) all contain
XX pancreatic (AAW01193) APLases have been partially sequenced
XX The sequences have been found to be highly homologous to a human
XX lymphoid cell activation antigen designated CD33 (Mitsunaka et
XX al. (1994) J. Immunol. 3574-3583). The complete sequences of the
XX APLases types I and II have not been determined. Assuming that
XX the CD33 gene product is an APLase type II, the use of CD33
XX in the reduction of platelet aggregation and of the at present
XX may be contemplated, as well as a process of making APLases
XX using the CD33 sequence (AAW01193)

XX
XX Sequence 20 AA;
XX
XX Query Match 2.1%; Score 9; DB 17; Length 20;
XX Best Local Similarity 100%; Pred. No. 0;
XX Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 159 LEUCASTO 205
XX
XX DB 11 LEUCASTO 19
XX
XX RESULT 40
XX AAU30879
XX ID AAU30879 standard; Protein: 141 AA
XX
XX AAU30879;
XX
XX 18-DEC-2001 (first entry)
XX
XX DE Novel human secreted protein #1370
XX
XX Human, vaccination gene therapy, nutritional supplement,
XX stem cell proliferation, haematopoiesis, nerve tissue regeneration,
XX immune suppression, immune stimulation, anti-inflammatory, leukemia
XX
XX Homo sapiens.
XX
XX WO200179449 A2;
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-050656
XX
XX 19-APR-2000; 2000US-065929
XX
XX 26-MAR-2001; 2001US-077016
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Dimanac RT;
XX
XX WPI: 2001-61702/70
XX
XX Nucleic acids encoding a range of human T lymphocytes, useful in gene
XX vaccination, testing and therapy.
XX
XX Claim 2, Page 347, 77FF, English
XX
XX The invention relates to novel human secreted polypeptides. The
XX polypeptides and antibodies to the polypeptides are useful for
XX determining the level of expression of a gene in a tissue, associated
XX with altered levels of expression. The polypeptides are also useful for
XX identifying agents (agonists and antagonists) that bind to them. Claim

XX expressing the proteins are useful for identifying a therapeutic agent
XX for use in treatment of a pathology related to aberrant expression of
XX physiological interactions of the polypeptide. The proteins comprising
XX the nucleic acids encoding the polypeptides and cells genetically
XX engineered to express them are also useful for producing the proteins.
XX The proteins are useful in genetic vaccination, testing and
XX therapy, and for the treatment of immunological suppression, allergy, and
XX increase stem cell proliferation, to regulate haematopoiesis, and to
XX bone, cartilage, tendon and/or nerve tissue growth or regeneration.
XX Immune suppression and/or stimulation, as anti-inflammatory agents, and
XX in treatment of leukemia, lymphoma, myeloid leukemia, and other acute
XX sequences of novel human secreted proteins of the invention.

XX
XX Sequence 10 AA;
XX
XX Query Match 0.1%; Score 0; DB 20; Length 141;
XX Best Local Similarity 100%; Pred. No. 1;
XX Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 336 FVAFSYVD 334
XX
XX DB 39 FVAFSYVD 47
XX
XX RESULT 41
XX AAB71918
XX ID AAB71918 standard; Protein: 439 AA.
XX
XX AAB71918;
XX
XX 09-MAY-2001 (first entry)
XX
XX DE Soluble human CD33 polypeptide.
XX
XX Homo sapiens. CD33, type II, is a member of the APLase family (Mitsunaka et
XX al. (1994) J. Immunol. 3574-3583). It is a type II APLase, which is
XX a type II APLase, which is a type II APLase, which is a type II APLase,
XX stroke, thrombotic disorder, leukocyte disorder.
XX
XX Homo sapiens.
XX
XX WO200119449 A2;
XX
XX 22-FEB-2001.
XX
XX 11-MAR-2000; 2000WO-US22660.
XX
XX 13-AUG-1999; 99US-0374586.
XX
XX (USCC) CIVIL COMMERCE NEW YORK.
XX
XX Pinsky DJ;
XX
XX WPI: 2001-202805/20.
XX
XX Treating stroke in a subject susceptible to intracranial hemorrhage;
XX and an ischemic disorder; methods administering a CD33 polypeptide
XX which inhibits APL mediated platelet aggregation or leukocyte
XX accumulation
XX
XX Claim 3, Page 14, 118FF, English.
XX
XX The present sequence is the active fragment of human CD33, type II, or its
XX active fragment may be administered to a subject to prevent stroke in a
XX subject susceptible to intracranial hemorrhage or an ischemic
XX disorder. The CD33 polypeptide inhibits APL-mediated platelet aggregation
XX or leukocyte accumulation, and is useful for identifying agents (agonists
XX and antagonists) that bind to it. The CD33 polypeptide is useful for
XX vascular disorder, pulmonary embolism, venous thrombosis, myocardial
XX infarction, thrombotic thrombocytopenic syndrome, unstable angina, peripheral
XX vascular disease, stroke, and other thrombotic disorders. The CD33
XX polypeptide is also useful for identifying agents (agonists and antagonists)
XX that bind to it. The CD33 polypeptide is also useful for identifying agents
XX (agonists and antagonists) that bind to it. The CD33 polypeptide is also
XX useful for identifying agents (agonists and antagonists) that bind to it.

FT Note: "soluble site of leader sequence"
 FT 35 473
 FT Protein /note: "Human soluble CD39 protein"
 XX
 XX W0200023459-A1.
 XX
 XX 27-APR-2000.
 XX
 XX 13-OCT-1999; 99W0-052966
 XX
 XX 16-OCT-1998; 98US-0134585.
 XX 06-NOV-1998; 98US-0137466.
 XX 13-AUG-1999; 99US-0149010.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Malszewski CR, Gayle RB, Price VL, Gimbel SD;
 XX WPI, 2000-339644/29.
 XX
 XX Now soluble CD39 polypeptides having affinity, activity, and function for
 XX inhibiting angiogenesis and promoting vascular injury, myocardial
 XX infarction, stroke, coronary artery disease or injury.
 XX
 XX Claim 6: Page 114-116; 100FF, English
 XX
 XX The present sequence is the fusion protein construct, consisting of the
 XX construct comprising of the leader peptide from human interleukin 2 (hIL2)
 XX and soluble CD39 (solCD39) protein region, having glycosylated activity.
 XX Soluble CD39 is constructed by removing the N and C-terminal
 XX transmembrane domains. It retains the capacity to mediate ATP and ADP
 XX at relevant concentrations and the ability to block and reverse
 XX ADP-induced platelet activation and aggregation in whole blood.
 XX Aggregation soluble CD39 polypeptides are useful for inhibiting
 XX angiogenesis. It is useful for the treatment of myocardial infarction,
 XX myocardial ischemia, coronary artery disease or injury, stroke,
 XX atherosclerosis, peripheral vascular circulation, pre-eclampsia, placental
 XX associated ischemic disorders including intra-uterine and neonatal
 XX ischemia, thrombotic disorders including coronary, peripheral and
 XX cerebral artery thrombosis, hemorrhagic and venous disorders, and
 XX coagulopathy, deep venous thrombosis, pulmonary embolism, and
 XX transient ischemic attack. Soluble CD39 is also useful for preventing
 XX thrombus formation in polymeric catheters, catheters for intravascular
 XX catheters of blood vessels or stroke.
 XX
 XX Sequence 473 AA:
 XX
 XX Query March 2, 1997 Score 9; DB 21; Length 473;
 XX Best Local Similarity 100.0%; Pred. No. 21;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 XX
 XX 198 LDDGASTG 206
 XX |||||
 XX 209 LDDGASTG 217
 XX
 XX RESULT 51
 XX AAY70900
 XX ID AAY70900 standard: Protein; 474 AA.
 XX
 XX AAY70900;
 XX
 XX 17-AUG-2000 (first entry)
 XX
 XX Protein encoded by Trm 3 construct.
 XX
 XX Soluble CD39: ADP-induced platelet aggregation, platelet aggregation,
 XX vascular injury, myocardial infarction, stroke, coronary artery disease,
 XX atherosclerosis, peripheral vascular circulation, pre-eclampsia, embolism,
 XX placental-associated ischemic disorder, lung ischemia, thrombolytic,
 XX cerebral ischemia, hemorrhagic disorders, deep venous thrombosis,
 XX pulmonary embolism, intravascular thrombosis, catheters for intravascular
 XX catheters of blood vessels, stroke, deep venous thrombosis, embolism,
 XX peripheral artery thrombosis, coagulopathy, deep venous thrombosis, embolism,
 XX

XX PE, platelet aggregation, myocardial infarction, stroke, coronary artery disease,
 XX atherosclerosis, peripheral vascular circulation, pre-eclampsia, embolism,
 XX placental-associated ischemic disorder, lung ischemia, thrombolytic,
 XX cerebral ischemia, hemorrhagic disorders, deep venous thrombosis,
 XX pulmonary embolism, intravascular thrombosis, catheters for intravascular
 XX catheters of blood vessels, stroke, deep venous thrombosis, embolism,
 XX peripheral artery thrombosis, coagulopathy, deep venous thrombosis, embolism,
 XX
 XX Homosapiens.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX FT Cleavage-site 24-25
 XX FT Protein 35-473
 XX FT Note: "soluble portion of CD39"
 XX
 XX W0200023394-A2.
 XX
 XX 27-APR-2000.
 XX
 XX 13-OCT-1999; 99W0-053441.
 XX
 XX 16-OCT-1998; 98US-0134585.
 XX 06-NOV-1998; 98US-0137466.
 XX 13-AUG-1999; 99US-0149010.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX (TRF) TRFED, INC.
 XX
 XX Malszewski CR, Gayle RB, Malszewski AD;
 XX WPI, 2000-339618/29.
 XX
 XX Inhibiting platelet activation and recruitment, useful for treating a
 XX normal suffering from vascular injury, myocardial infarction, stroke,
 XX coronary artery disease or injury, coagulation abnormalities and
 XX polypeptides.
 XX
 XX Example 11: Page 113-114; 100FF, English.
 XX
 XX The present sequence is the protein encoded by Trm 3 construct, consisting of
 XX the leader peptide from human interleukin 2 (hIL2) and soluble CD39 (solCD39)
 XX polypeptide region, having glycosylated activity.
 XX Soluble CD39 is constructed by removing the N and C-terminal
 XX transmembrane domains. It retains the capacity to mediate ATP and ADP
 XX at relevant concentrations and the ability to block and reverse
 XX ADP-induced platelet activation and aggregation in whole blood.
 XX Aggregation soluble CD39 polypeptides are useful for inhibiting
 XX angiogenesis. It is useful for the treatment of myocardial infarction,
 XX myocardial ischemia, coronary artery disease or injury, stroke,
 XX atherosclerosis, peripheral vascular circulation, pre-eclampsia, placental
 XX associated ischemic disorders including intra-uterine and neonatal
 XX ischemia, thrombotic disorders including coronary, peripheral and
 XX cerebral artery thrombosis, hemorrhagic and venous disorders, and
 XX coagulopathy, deep venous thrombosis, pulmonary embolism, and
 XX transient ischemic attack. Soluble CD39 is also useful for preventing
 XX thrombus formation in polymeric catheters, catheters for intravascular
 XX catheters of blood vessels or stroke.
 XX
 XX Sequence 474 AA:
 XX
 XX Query March 2, 1997 Score 9; DB 21; Length 474;
 XX Best Local Similarity 100.0%; Pred. No. 21;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 XX
 XX 198 LDDGASTG 206
 XX |||||
 XX 210 LDDGASTG 218
 XX
 XX RESULT 52
 XX AAY70923
 XX ID AAY70923 standard: Protein; 474 AA.
 XX
 XX AAY70923;
 XX
 XX 17-AUG-2000 (first entry)
 XX

XX 13-OCT-1999; 99WS-0914541.
 XX 16-OCT-1999; 99WS-0104585.
 XX 06-NOV-1999; 99WS-0107446.
 XX 13-AUG-1999; 99WS-0104010.
 XX (IMMV) IMMUNEX CORP.
 XX (CORP) CORPHEM RES FORM INC.
 XX Maliszewski CR, Gayle RB, Marcus AJ;
 XX WPI: 2000.339519/29.
 XX N.PSRN: AAD00204.
 XX Inhibiting platelet activation and recruitment, useful for treating a
 XX mammal suffering from unstable angina, myocardial infarction, stroke,
 XX coronary artery disease, or injury associated with thrombotic disorders
 XX polypeptides -
 XX Example 9: Page 109-111; 118pp; English.
 XX The present sequence is embodied by soluble CD39 (soluble CD39) expression
 XX plasmid. This was used for the transient expression of soluble protein in
 XX mammalian expression systems. Soluble CD39 is used in the treatment of
 XX unstable angina, myocardial infarction, stroke, coronary artery disease,
 XX or injury associated with thrombotic disorders including lung
 XX embolism, platelet-associated ischemic disorders including lung
 XX embolism, coronary artery disease and cerebral ischemia. The soluble protein
 XX including CD39 is used in the treatment of thrombotic disorders including
 XX intracerebral thrombotic, peripheral artery thrombotic, venous thrombotic,
 XX thrombotic, coagulopathy, deep venous thrombosis (DVT), pulmonary
 XX embolism (PE), transient ischemic attack. Soluble CD39 is also useful
 XX for preventing thrombus formation in patients with cardiovascular disorders
 XX stenosis or reformation of blood vessels or stroke.
 XX Sequence 487 AA;
 XX
 XX Query Match: 21% Score 9, E-21, Length 487,
 XX Best Local Similarity: 100.0%, Field No. 2.5,
 XX Barcodes: 0, Conservative: 0, Mismatch: 0, Indels: 0, Gaps: 0
 XX
 XX 108 IDLQASTQ 206
 XX 223 IDLQASTQ 231
 XX
 XX RESULT 58
 XX AAY70921
 XX ID AAY70921 standard; Protein; 487 AA;
 XX AAY70921,
 XX
 XX 17-AUG-2000 (first entry)
 XX
 XX Human soluble CD39 fusion protein construct, F110F1038210201.
 XX Soluble CD39 (soluble human) hydropathy activity, platelet activation,
 XX unstable angina, myocardial infarction, stroke, coronary artery disease,
 XX atherosclerosis, peripheral vascular disease, thrombotic disorders, lung
 XX embolism-associated ischemic disorders, thrombotic disorders, coronary artery
 XX disease, deep venous thrombosis, pulmonary embolism, stroke, stroke
 XX transient ischemic attack, stroke, stroke, stroke, stroke, stroke, stroke,
 XX intracerebral thrombotic, peripheral artery thrombotic, venous thrombotic,
 XX thrombotic, coagulopathy, deep venous thrombosis (DVT), pulmonary embolism (PE),
 XX transient ischemic attack, stroke, stroke, stroke, stroke, stroke, stroke,
 XX thrombus formation or reformation, occlusion, reocclusion, stenosis or
 XX stenosis of blood vessels or stroke.
 XX
 XX CS Homo sapiens
 XX CS Synthetic.
 XX
 XX Key location/Qualifiers
 XX FH 1..24
 XX FT Peptide
 XX FT /label: leader peptide
 XX FT /note: "Derived from human interleukin 2 (IL2)"

XX Peptide 25..36
 XX /note: "Mouse human interleukin 2 (IL2) (1-36)"
 XX Region 37..40
 XX /note: "linker sequence"
 XX Region 41..48
 XX /note: "FLAG Tag sequence"
 XX Protein 49..487
 XX /note: "Human soluble CD39 protein"
 XX
 XX W020023459-A1.
 XX
 XX 27-APR-2000.
 XX
 XX 13-OCT-1999; 99WS-0922955.
 XX
 XX 16-OCT-1999; 99WS-0104585.
 XX 06-NOV-1999; 99WS-0107446.
 XX 13-AUG-1999; 99WS-0104010.
 XX
 XX (IMMV) IMMUNEX CORP.
 XX
 XX Maliszewski CR, Gayle RB, Price VL, Gimpel SC;
 XX WPI: 2000.339519/29.
 XX N.PSRN: AAD00209.
 XX
 XX How soluble CD39 polypeptides having apyrase activity, useful for
 XX inhibiting angiogenesis and treating vascular-related diseases, myocardial
 XX infarction, stroke, coronary artery disease or injury
 XX polypeptides -
 XX Example 9: Page 109-111; 122pp; English.
 XX
 XX The present sequence is the fusion protein construct F110F1038210201,
 XX comprising the leader peptide, the soluble CD39 polypeptide, and the linker
 XX and FLAG tag. The soluble CD39 polypeptide is used in the treatment of
 XX unstable angina, myocardial infarction, stroke, coronary artery disease, and
 XX stroke. Soluble CD39 (soluble CD39) protein region that has apyrase activity, that
 XX produces high levels of soluble cytosol and a highly active
 XX translocated cells. Soluble CD39 is constructed by joining the N- and
 XX C-terminal transmembrane domains. It retains the apyrase activity and
 XX AIT and AIT at the C-terminal domain and the AIT and AIT at the N-
 XX terminal domain. The soluble CD39 polypeptide is used in the treatment of
 XX unstable angina, myocardial infarction, stroke, coronary artery disease, and
 XX stroke. Soluble CD39 polypeptides are used for inhibiting
 XX platelet aggregation, soluble CD39 polypeptides are used for inhibiting
 XX angiogenesis. It is useful for the treatment of unstable angina,
 XX myocardial infarction, stroke, coronary artery disease or injury,
 XX atherosclerosis, peripheral vascular disease, thrombotic disorders, lung
 XX embolism-associated ischemic disorders including lung embolism and
 XX cerebral ischemia, thrombotic disorders including coronary artery, peripheral
 XX and cerebral artery thrombotic, intracerebral and venous thrombotic,
 XX coagulopathy, deep venous thrombotic (DVT), pulmonary embolism (PE),
 XX transient ischemic attack, stroke, stroke, stroke, stroke, stroke, stroke,
 XX thrombus formation or reformation, occlusion, reocclusion, stenosis or
 XX stenosis of blood vessels or stroke.
 XX
 XX CS Sequence 487 AA;
 XX
 XX Query Match: 21% Score 9, E-21, Length 487,
 XX Best Local Similarity: 100.0%, Field No. 2.5,
 XX Barcodes: 0, Conservative: 0, Mismatch: 0, Indels: 0, Gaps: 0
 XX
 XX 108 IDLQASTQ 206
 XX 223 IDLQASTQ 231
 XX
 XX RESULT 59
 XX AAY33296
 XX ID AAY33296 standard; Protein; 486 AA;
 XX AAY33296,
 XX
 XX 26-NOV-1999 (first entry)
 XX
 XX Human membrane spanning protein MSP-3.

XX 13-JUL-2000.
 PD 07-JAN 2000; 2000WO US00466.
 XX
 PR 08-JAN 1999; 99US 0115293.
 XX
 PA (CERE-) CERES INC.
 XX
 PI Alexander N. Brover V, Chen X, Subramanian S, Trenchard ME,
 PI Zheng L;
 XX
 DF WPI: 2000-465970/40
 XX
 PT New corn plant and Arabidopsis thaliana sequence determined DNA
 fragments, useful for expressing gene products and for controlling
 PT expression of a target gene.
 XX
 PS Claim 14; Page 469; 673pp; English.
 XX
 CC The present invention describes polynucleotides, such as complete cDNA
 CC sequences and/or sequences of genomic DNA encompassing complete genes,
 CC portions of genes, and/or intergenic regions, collectively referred to
 CC as sequence-determined DNA fragments (SDNF), from corn plants and
 CC Arabidopsis thaliana. The SDNFs are promoters, structural genes,
 CC untranslated regions (UTRs), or 3' terminal sequences. They can be
 CC used for expressing a gene product and controlling expression of a
 CC target gene, either as a promoter, a structural gene, or as a
 CC 3' terminal sequence. They are also useful as tools for genetic
 CC mapping, and identification of a particular individual plant or for
 CC clustering a group of plants with a common trait. AAT4943 to AAT78630
 CC and AAT4943 to AAT78630 represent two specifically identified
 CC polynucleotide sequences and polypeptides encoded by them given in the
 CC present invention.
 XX
 SO Sequence 151 AA;
 Query Match 1.98; Score 8; DB 21; Length 151;
 Best Local Similarity 100.0%; Prod. No. 12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CY 128 KATACLRPL 135
 DB 100 KATACLRPL 107
 RESULT 73
 AAB24732
 ID AAB24732 standard, Peptide, 103 AA.
 XX
 AC AAB24732;
 XX
 DT 27 NOV 2000 (first entry)
 XX
 DE Plant SDF encoded polypeptide sequence SEQ list 1 N(117).
 XX
 KW Plant, corn, Arabidopsis thaliana, sequence-determined DNA fragments,
 KW SDF, genetic mapping, identification, promoter, structural gene, UTR,
 KW untranslated region, expression control
 XX
 OS Plant.
 XX
 PE W000094056 A0
 XX
 PD 13-JUL-2000.
 XX
 PF (7-JAN 2000; 2000WO US00466.
 XX
 PR 08-JAN 1999; 99US 0115293
 XX
 PA (CERE-) CERES INC.
 XX
 PI Alexander N, Brover V, Chen X, Subramanian S, Trenchard ME,
 PI Zheng L;

PI Zheng L;
 XX
 DR WPI: 2000-465970/40.
 XX
 PT New corn plant and Arabidopsis thaliana sequence determined DNA
 PT fragments, useful for expressing gene products and for controlling
 PT expression of a target gene.
 XX
 PS Claim 14; Page 408-409; 673pp; English.
 XX
 CC The present invention describes polynucleotides, such as complete cDNA
 CC sequences and/or sequences of genomic DNA encompassing complete genes,
 CC portions of genes, and/or intergenic regions, collectively referred to
 CC as sequence-determined DNA fragments (SDNF), from corn plants and
 CC Arabidopsis thaliana. The SDNFs are promoters, structural genes,
 CC untranslated regions (UTRs), or 3' terminal sequences. They can be
 CC used for expressing a gene product and controlling expression of a
 CC target gene, either as a promoter, a structural gene, or UTR or as a
 CC 3' terminal sequence. They are also useful as tools for genetic
 CC mapping, and identification of a particular individual plant or for
 CC clustering a group of plants with a common trait. AAT4943 to AAT78630
 CC and AAT4943 to AAT78630 represent two specifically identified
 CC polynucleotide sequences and polypeptides encoded by them given in the
 CC present invention.
 XX
 SO Sequence 153 AA;
 Query Match 1.98; Score 8; DB 21; Length 153;
 Best Local Similarity 100.0%; Prod. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CY 128 KATACLRPL 135
 DB 79 KATACLRPL 86
 RESULT 74
 AAB24731
 ID AAB24731 standard, Peptide, 100 AA.
 XX
 AC AAB24731;
 XX
 DT 27-NOV-2000 (first entry)
 XX
 DE Plant SDF encoded polypeptide sequence SEQ list 1 N(117).
 XX
 KW Plant, corn, Arabidopsis thaliana, sequence-determined DNA fragments,
 KW SDF, genetic mapping, identification, promoter, structural gene, UTR,
 KW untranslated region, expression control.
 XX
 OS Plant.
 XX
 PE W000094056 A0.
 XX
 PD 13-JUL-2000.
 XX
 PF (7-JAN 2000; 2000WO US00466.
 XX
 PR 08-JAN-1999; 99US 0115293.
 XX
 PA (CERE-) CERES INC.
 XX
 PI Alexander N, Brover V, Chen X, Subramanian S, Trenchard ME,
 PI Zheng L;
 XX
 DR WPI: 2000-465970/40.
 XX
 PT New corn plant and Arabidopsis thaliana sequence determined DNA
 PT fragments, useful for expressing gene products and for controlling
 PT expression of a target gene.
 XX
 PS Claim 14; Page 408; 673pp; English.

1

2

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OM protein - protein search, using sw model

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RUN ON:          Time 00, 2023, 14:56:34 ; Session time 27 Seconds  
                (without alignments)  
                1798106 MIPs = 1798106 Reads
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US-09-905-744R-6

Perfect score: 428
Sequence: 1 MATWGVTFMVLVSCVCSA.....ETGNALISA¹PHLQSLQISH 428

Scoring table: OLIGO

$$G\Gamma_n = \Gamma \quad \text{and} \quad G\Gamma_{n+1} = \Gamma$$

Searchad 424659 3092 10569623 20010000

Word size

Received 10/10/2016

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Minimum DB seq length: 0
Maximum FR seq length: 2000000000
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Post-processing: listing first 10 summaries

Database : Published Applications AA:

[illegible]

Prof. M. B. is the author of several books and articles on the score method, than or equal to the score of the leader being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Sec.	Chry.	Length	TR	IR	Alt.	Loc.
1	4	1	1	4	1	1	1	1
2	4	1	1	4	1	1	1	1
3	4	1	1	4	1	1	1	1
4	4	1	1	4	1	1	1	1
5	4	1	1	4	1	1	1	1
6	4	1	1	4	1	1	1	1
7	4	1	1	4	1	1	1	1
8	4	1	1	4	1	1	1	1
9	4	1	1	4	1	1	1	1
10	4	1	1	4	1	1	1	1
11	4	1	1	4	1	1	1	1
12	4	1	1	4	1	1	1	1
13	4	1	1	4	1	1	1	1
14	4	1	1	4	1	1	1	1
15	4	1	1	4	1	1	1	1
16	4	1	1	4	1	1	1	1
17	4	1	1	4	1	1	1	1
18	4	1	1	4	1	1	1	1
19	4	1	1	4	1	1	1	1
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[illegible]

RESULT 29

US-10-176-913-496

Sequence 496, Application US/10176913

Publication No. US20030022398A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUESTERED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIDE

FILE REFERENCE: P3430P1066

CURRENT APPLICATION NUMBER: US/10/176-913

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 459

TYPE: PPT

ORGANISM: Homo Sapien

US-10-176-913-496

Query Match 2.1% Score 9, DB 9, Length 459,
 Best Local Similarity 100.0%, Pred. No. 2, 9,
 Matches 9, Conservative 0, Mismatches 0, Totals 0, Gaps 0

201 GGAATGTTT 209

207 GGAATGTTT 215

RESULT 29

US-10-180-552-496

Sequence 496, Application US/10180552

Publication No. US20030022398A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUESTERED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIDE

FILE REFERENCE: P3430P1066

CURRENT APPLICATION NUMBER: US/10/180-552

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 459

TYPE: PPT

ORGANISM: Homo Sapien

US-10-180-552-496

Query Match 2.1% Score 9, DB 9, Length 459,
 Best Local Similarity 100.0%, Pred. No. 2, 9,
 Matches 9, Conservative 0, Mismatches 0, Totals 0, Gaps 0

201 GGAATGTTT 209

201 GGAATGTTT 215

RESULT 30

US-10-180-557-496

Sequence 496, Application US/10180557

Publication No. US20030022398A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUESTERED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIDE

FILE REFERENCE: P3430P1066

CURRENT APPLICATION NUMBER: US/10/180-557

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 458

TYPE: PPT

ORGANISM: Homo Sapien

US-10-180-557-496

Query Match 2.1% Score 9, DB 9, Length 458,
 Best Local Similarity 100.0%, Pred. No. 2, 9,
 Matches 9, Conservative 0, Mismatches 0, Totals 0, Gaps 0

201 GGAATGTTT 209

207 GGAATGTTT 215

RESULT 31

US-10-173-700-496

Sequence 496, Application US/10173700

Publication No. US20030022398A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUESTERED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIDE

FILE REFERENCE: P3430P1066

CURRENT APPLICATION NUMBER: US/10/173-700

CURRENT FILING DATE: 2002-06-17

Prior Application removed - See file wrapper or Palm

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 496

LENGTH: 458

TYPE: PPT

ORGANISM: Homo Sapien

US-10-173-700-496

Query Match 2.1% Score 9, DB 9, Length 458,
 Best Local Similarity 100.0%, Pred. No. 2, 9,
 Matches 9, Conservative 0, Mismatches 0, Totals 0, Gaps 0

201 GGAATGTTT 209

Matches 92 Conserved 92 Mismatched 0 Indels 0 Gaps 0

Query 201 GASTGCTF 215

DB 207 GASTGCTF 215

RESULT 42

US-10-174-572-496

Sequence 496, Application US/10174572

Publication No. US200302766A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Yan

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Guinney, Austin

APPLICANT: Pan, James

APPLICANT: Smith, Victor

APPLICANT: Watanabe, Colin R.

APPLICANT: Wood, William L.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEPTIN AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL

FILE REFERENCE: P4408134

CURRENT FILING DATE: 2002/06/18

TITLE OF INVENTION: SEPTIN AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL

FILE REFERENCE: P4408134

CURRENT FILING DATE: 2002/06/18

PILOT APPLICATION REMOVED: See File Wrapper at Palm

SEQ ID NO 496

LENGTH: 496

TYPE: PRT

ORGANISM: Homo sapiens

US-10-174-572-496

Query Match

Best Local Similarity: 100.0% Ident. No. 292

Matches 92 Conserved 92 Mismatched 0 Indels 0 Gaps 0

US-10-174-572-496

Sequence 496, Application US/10174572

Publication No. US200302766A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Yan

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Guinney, Austin

APPLICANT: Pan, James

APPLICANT: Smith, Victor

APPLICANT: Watanabe, Colin R.

APPLICANT: Wood, William L.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEPTIN AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL

FILE REFERENCE: P4408134

CURRENT FILING DATE: 2002/06/18

TITLE OF INVENTION: SEPTIN AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL

FILE REFERENCE: P4408134

CURRENT FILING DATE: 2002/06/18

PILOT APPLICATION REMOVED: See File Wrapper at Palm

SEQ ID NO 496

LENGTH: 496

TYPE: PRT

ORGANISM: Homo sapiens

US-10-174-572-496

Query Match

Best Local Similarity: 100.0% Ident. No. 292

Matches 92 Conserved 92 Mismatched 0 Indels 0 Gaps 0

US-10-174-582-496

Sequence 496, Application US/10174582

Publication No. US200302766A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Yan

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Guinney, Austin

APPLICANT: Pan, James

APPLICANT: Smith, Victor

APPLICANT: Watanabe, Colin R.

APPLICANT: Wood, William L.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEPTIN AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL

FILE REFERENCE: P4408134

CURRENT FILING DATE: 2002/06/18

TITLE OF INVENTION: SEPTIN AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL

FILE REFERENCE: P4408134

CURRENT FILING DATE: 2002/06/18

PILOT APPLICATION REMOVED: See File Wrapper at Palm

SEQ ID NO 496

LENGTH: 496

TYPE: PRT

ORGANISM: Homo sapiens

US-10-174-582-496

Query Match

Best Local Similarity: 100.0% Ident. No. 292

Matches 92 Conserved 92 Mismatched 0 Indels 0 Gaps 0

US-10-174-582-496

Sequence 496, Application US/10174582

Publication No. US200302766A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Yan

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Guinney, Austin

APPLICANT: Pan, James

APPLICANT: Smith, Victor

APPLICANT: Watanabe, Colin R.

APPLICANT: Wood, William L.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEPTIN AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL

FILE REFERENCE: P4408134

CURRENT FILING DATE: 2002/06/18

TITLE OF INVENTION: SEPTIN AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL

FILE REFERENCE: P4408134

CURRENT FILING DATE: 2002/06/18

PILOT APPLICATION REMOVED: See File Wrapper at Palm

SEQ ID NO 496

LENGTH: 496

TYPE: PRT

ORGANISM: Homo sapiens

US-10-174-582-496

TYPE: PRT
ORGANISM: Homo Sapien
US-10-174-588-496

Query Match 2.1% Score 9, DB 9, Length 458,
Best Local Similarity 100.0%, Prod. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0,

QY 201 GGASTCTF 209
DB 207 GGASTCTF 215

RESULT 36
US-10-175-739-496

Sequence 496, Application US/10175739
Publication No. US2003027267A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jiah
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: DELETED AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL
TITLE OF INVENTION: AGES ENCODING THE SAME

FILE REFERENCE: P343091046

CURRENT APPLICATION NUMBER: 10/061775-739

CURRENT FILING DATE: 2002-06-16

Prior Application removed - See File Wrapper of Entry

INVENTOR: P. 209 10/061775-739

SEQ ID NO 496

LENGTH 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-175-739-496

Query Match 2.1% Score 9, DB 9, Length 458,
Best Local Similarity 100.0%, Prod. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0,

QY 201 GGASTCTF 209
DB 207 GGASTCTF 215

RESULT 37
US-10-175-740-496

Sequence 496, Application US/10175740
Publication No. US2003030268A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jiah
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: DELETED AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL
TITLE OF INVENTION: AGES ENCODING THE SAME

FILE REFERENCE: P343091046

CURRENT APPLICATION NUMBER: 10/061775-740

CURRENT FILING DATE: 2002-06-16

Prior Application removed - See File Wrapper of Entry

NUMBER OF SEQ ID NOS: 612
SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-740-496

Query Match 2.1% Score 9, DB 9, Length 458,
Best Local Similarity 100.0%, Prod. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0,

QY 201 GGASTCTF 209
DB 207 GGASTCTF 215

RESULT 38
US-10-175-743-496

Sequence 496, Application US/10175743
Publication No. US2003027267A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jiah
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: DELETED AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL
TITLE OF INVENTION: AGES ENCODING THE SAME

FILE REFERENCE: P343091046

CURRENT APPLICATION NUMBER: 10/061775-743

CURRENT FILING DATE: 2002-06-16

Prior Application removed - See File Wrapper of Entry

INVENTOR: P. 209 10/061775-743

SEQ ID NO 496

LENGTH 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-175-743-496

Query Match 2.1% Score 9, DB 9, Length 458,
Best Local Similarity 100.0%, Prod. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0,

QY 201 GGASTCTF 209
DB 207 GGASTCTF 215

RESULT 39
US-10-175-746-496

Sequence 496, Application US/10175746
Publication No. US2003030268A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jiah
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.

TITLE OF INVENTION: DELETED AND TRANSMEMBRANE POLYPEPTIDES AND NOVEL
TITLE OF INVENTION: AGES ENCODING THE SAME

FILE REFERENCE: P343091046

CURRENT APPLICATION NUMBER: 10/061775-746

CURRENT FILING DATE: 2002-06-16

Prior Application removed - See File Wrapper of Entry

Query Match 2.1% Score 9; DB 9; Length 459;
 Best Local Similarity: 100.0%; Filed: No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGASTOTTF 209
 |||||
 DB 207 GGASTOTTF 215

RESULT 39
 US-10-176-488-496

Sequence 496, Application US/10176488
 Publication No. US2003022721A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Andrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FILTRATION AND METHODS
 FILE REFERENCE: P443010119
 CURRENT APPLICATION NUMBER: US/10176488
 PRIORITY FILING DATE: 2002-06-21
 PRIOR APPLICATION REMOVED - See File Wrapper of P443010119
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 496
 LENGTH: 459
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-488-496

Query Match 2.1% Score 9; DB 9; Length 459;
 Best Local Similarity: 100.0%; Filed: No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGASTOTTF 209
 |||||
 DB 207 GGASTOTTF 215

RESULT 40
 US-10-176-492-496

Sequence 496, Application US/10176492
 Publication No. US2003022722A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Andrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FILTRATION AND METHODS
 FILE REFERENCE: P443010107
 CURRENT APPLICATION NUMBER: US/10176492
 PRIORITY FILING DATE: 2002-06-21
 PRIOR APPLICATION REMOVED - See File Wrapper of P443010107
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 496
 LENGTH: 459
 TYPE: PRT

ORGANISM: Homo Sapien
 US-10-176-492-496

Query Match 2.1% Score 9; DB 9; Length 459;
 Best Local Similarity: 100.0%; Filed: No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGASTOTTF 209
 |||||
 DB 207 GGASTOTTF 215

RESULT 41
 US-10-176-747-496

Sequence 496, Application US/10176747
 Publication No. US2003022721A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Andrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FILTRATION AND METHODS
 FILE REFERENCE: P443010102
 CURRENT APPLICATION NUMBER: US/10176747
 PRIORITY FILING DATE: 2002-06-21
 PRIOR APPLICATION REMOVED - See File Wrapper of P443010102
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 496
 LENGTH: 459
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-747-496

Query Match 2.1% Score 9; DB 9; Length 459;
 Best Local Similarity: 100.0%; Filed: No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 GGASTOTTF 209
 |||||
 DB 207 GGASTOTTF 215

RESULT 42
 US-10-176-750-496

Sequence 496, Application US/10176750
 Publication No. US2003022721A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Andrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE FILTRATION AND METHODS
 FILE REFERENCE: P443010103
 CURRENT APPLICATION NUMBER: US/10176750
 PRIORITY FILING DATE: 2002-06-21
 PRIOR APPLICATION REMOVED - See File Wrapper of P443010103
 NUMBER OF SEQ ID NOS: 612

TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P44301000
 CURRENT APPLICATION NUMBER: 02/07/170,000
 CURRENT FILING DATE: 2002/06/21
 PRIOR APPLICATION REMOVED - See File Wrapper of P44301000
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-993-496

Query Match 2.1% Score 97 DB 97 Length 458
 Best Local Similarity: 100.00, Pct ID: 100.00
 Matches 97 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 201 GGASTOTIF 209
 DB 207 GGASTOTIF 215

RESULT 47

US-10-176-993-496
 Sequence 496, Application US/10176993
 Publication No. US2003003290A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Guiney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND HOSTS
 FILE REFERENCE: P44301000
 CURRENT APPLICATION NUMBER: 02/07/170,000
 CURRENT FILING DATE: 2002/06/21
 PRIOR APPLICATION REMOVED - See File Wrapper of P44301000
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-993-496

Query Match 2.1% Score 97 DB 97 Length 458
 Best Local Similarity: 100.00, Pct ID: 100.00
 Matches 97 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 201 GGASTOTIF 209
 DB 207 GGASTOTIF 215

RESULT 48

US-10-184-658-496
 Sequence 496, Application US/10184658
 Publication No. US2003002728A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Guiney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND HOSTS
 FILE REFERENCE: P44301000
 CURRENT APPLICATION NUMBER: US/10176,993
 CURRENT FILING DATE: 2002/06/21
 PRIOR APPLICATION REMOVED - See File Wrapper of P44301000
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-176-993-496

Query Match 2.1% Score 97 DB 97 Length 458
 Best Local Similarity: 100.00, Pct ID: 100.00
 Matches 97 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 201 GGASTOTIF 209
 DB 207 GGASTOTIF 215

RESULT 49

US-10-173-695-496
 Sequence 496, Application US/10173695
 Publication No. US2003003210A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Guiney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND HOSTS
 FILE REFERENCE: P44301000
 CURRENT APPLICATION NUMBER: US/10173,695
 CURRENT FILING DATE: 2002/06/17
 PRIOR APPLICATION REMOVED - See File Wrapper of P44301000
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO: 496
 LENGTH: 458
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-173-695-496

Query Match 2.1% Score 97 DB 97 Length 458
 Best Local Similarity: 100.00, Pct ID: 100.00
 Matches 97 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 201 GGASTOTIF 209
 DB 207 GGASTOTIF 215

RESULT 50

US-10-173-695-496
 Sequence 496, Application US/10173695
 Publication No. US2003003210A1
 GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Guiney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin


```

/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria K.
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
/ FILE REFERENCE: P4309109
/ CURRENT APPLICATION NUMBER: US/01/76,496
/ PRIORITY FILING DATE: 2002-06-20
/ PRIOR APPLICATION REMOVED - See file wrapper of P4309109
/ NUMBER OF SEQ ID NOS: 613
/ SEQ ID NO: 496
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-485-496

```

```

Query Match          2.1%, Score 9, DB 9, Length 458,
Best Local Similarity 100.0%, Freq. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

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QY 201 GGAAGTCITF 209
DB 207 GGAAGTCITF 215

```

```

RESULT 58
US-10-176-487-496
/ Sequence 496, Application US/01/76487
/ Publication No. US2003032110A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Godard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
/ FILE REFERENCE: P4309109
/ CURRENT APPLICATION NUMBER: US/01/76,496
/ PRIORITY FILING DATE: 2002-06-20
/ PRIOR APPLICATION REMOVED - See file wrapper of P4309109
/ NUMBER OF SEQ ID NOS: 613
/ SEQ ID NO: 496
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-487-496

```

```

Query Match          2.1%, Score 9, DB 9, Length 458,
Best Local Similarity 100.0%, Freq. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

```

QY 201 GGAAGTCITF 209
DB 207 GGAAGTCITF 215

```

```

RESULT 59
US-10-176-493-496
/ Sequence 496, Application US/01/76493
/ Publication No. US200303211A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.

```

```

/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Godard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
/ FILE REFERENCE: P4309109
/ CURRENT APPLICATION NUMBER: US/01/76,493
/ PRIORITY FILING DATE: 2002-06-20
/ PRIOR APPLICATION REMOVED - See file wrapper of P4309109
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO: 496
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-493-496

```

```

Query Match          2.1%, Score 9, DB 9, Length 458,
Best Local Similarity 100.0%, Freq. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

```

QY 201 GGAAGTCITF 209
DB 207 GGAAGTCITF 215

```

```

RESULT 60
US-10-176-756-496
/ Sequence 496, Application US/01/76756
/ Publication No. US2003032112A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Godard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND USES
/ FILE REFERENCE: P4309109
/ CURRENT APPLICATION NUMBER: US/01/76,756
/ PRIORITY FILING DATE: 2002-06-21
/ PRIOR APPLICATION REMOVED - See file wrapper of P4309109
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO: 496
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-176-756-496

```

```

Query Match          2.1%, Score 9, DB 9, Length 458,
Best Local Similarity 100.0%, Freq. No. 2.9,
Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

```

```

QY 201 GGAAGTCITF 209
DB 207 GGAAGTCITF 215

```

```

RESULT 61
US-10-176-911-496
/ Sequence 496, Application US/01/76911

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DL 207 GGASTOTIF 215

RESULT 65
US-10-179-510-496

Sequence 496, Application US/10196510
Publication No. US2003032117A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND METHODS

FILE REFERENCE: P3430P1018

CURRENT APPLICATION NUMBER: US/10196510

CURRENT FILING DATE: 2002-06-24

PRIOR APPLICATION REMOVED - See File Wrapper of this

SEQUENCE OF SEQ ID NOS: 612

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-179-510-496

Query Match Best Local Similarity: 100.0% Score 9, DB 9, Length 458

Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

DL 207 GGASTOTIF 215

RESULT 66
US-10-180-543-496

Sequence 496, Application US/10190543
Publication No. US2003032118A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND METHODS

FILE REFERENCE: P3430P1018

CURRENT APPLICATION NUMBER: US/10190543

CURRENT FILING DATE: 2002-06-25

PRIOR APPLICATION REMOVED - See File Wrapper of this

SEQUENCE OF SEQ ID NOS: 612

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-180-543-496

Query Match Best Local Similarity: 100.0% Score 9, DB 9, Length 458

Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

DL 207 GGASTOTIF 209

RESULT 67
US-10-180-544-496

Sequence 496, Application US/10190544
Publication No. US2003032119A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND METHODS

FILE REFERENCE: P3430P1018

CURRENT APPLICATION NUMBER: US/10190544

CURRENT FILING DATE: 2002-06-25

PRIOR APPLICATION REMOVED - See File Wrapper of this

SEQUENCE OF SEQ ID NOS: 612

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-180-544-496

Query Match Best Local Similarity: 100.0% Score 9, DB 9, Length 458

Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

DL 207 GGASTOTIF 215

RESULT 68
US-10-180-546-496

Sequence 496, Application US/10190546
Publication No. US2003032120A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin F.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: SEQUENCED AND TRANSMEMBRANE POLYPEPTIDES AND METHODS

FILE REFERENCE: P3430P1018

CURRENT APPLICATION NUMBER: US/10190546

CURRENT FILING DATE: 2002-06-25

PRIOR APPLICATION REMOVED - See File Wrapper of this

SEQUENCE OF SEQ ID NOS: 612

LENGTH: 458

TYPE: PRT

ORGANISM: Homo Sapien

US-10-180-546-496

Query Match Best Local Similarity: 100.0% Score 9, DB 9, Length 458

Matches 9, Conservative 0, Mismatches 0, Indels 0, Gaps 0

SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-180-559-496

Query Match 2.1% Score 0. DB 0. Length 458
Best Local Similarity 100%, File No. 2.9
Matches 0. Conservative 0. Mismatches 0. Indels 0. Gaps 0.

CV 201 GGASTQITF 209
|||||
DB 207 GGASTQITF 215

RESULT 73
US-10-181-000-496
Sequence 496, Application US/10181000
Publication No. US2000021056A1

GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desrochers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Galswsky, Paul J.
APPLICANT: Gurney, Austin I.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND NUMBER
TITLE OF INVENTION: ACTS ENCODING THE SAME
FILE REFERENCE: P43091017 US/01/01/000
CURRENT AFFILIATION NUMBER: 60/054263
PRIORITY FILING DATE: 1997-06-26
PRIORITY APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 012
SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-181-000-496

Query Match 2.1% Score 0. DB 0. Length 458
Best Local Similarity 100%, File No. 2.9
Matches 0. Conservative 0. Mismatches 0. Indels 0. Gaps 0.

CV 201 GGASTQITF 209
|||||
DB 207 GGASTQITF 215

RESULT 74
US-10-183-010-496
Sequence 496, Application US/10183010
Publication No. US2000021056A1
GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desrochers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Galswsky, Paul J.
APPLICANT: Gurney, Austin I.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND NUMBER
TITLE OF INVENTION: ACTS ENCODING THE SAME
FILE REFERENCE: P43091017 US/01/01/000
CURRENT AFFILIATION NUMBER: 60/054263

CURRENT FILING DATE: 2002-06-26
PRIORITY APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-183-010-496

Query Match 2.1% Score 0. DB 0. Length 458
Best Local Similarity 100%, File No. 2.9
Matches 0. Conservative 0. Mismatches 0. Indels 0. Gaps 0.

CV 201 GGASTQITF 209
|||||
DB 207 GGASTQITF 215

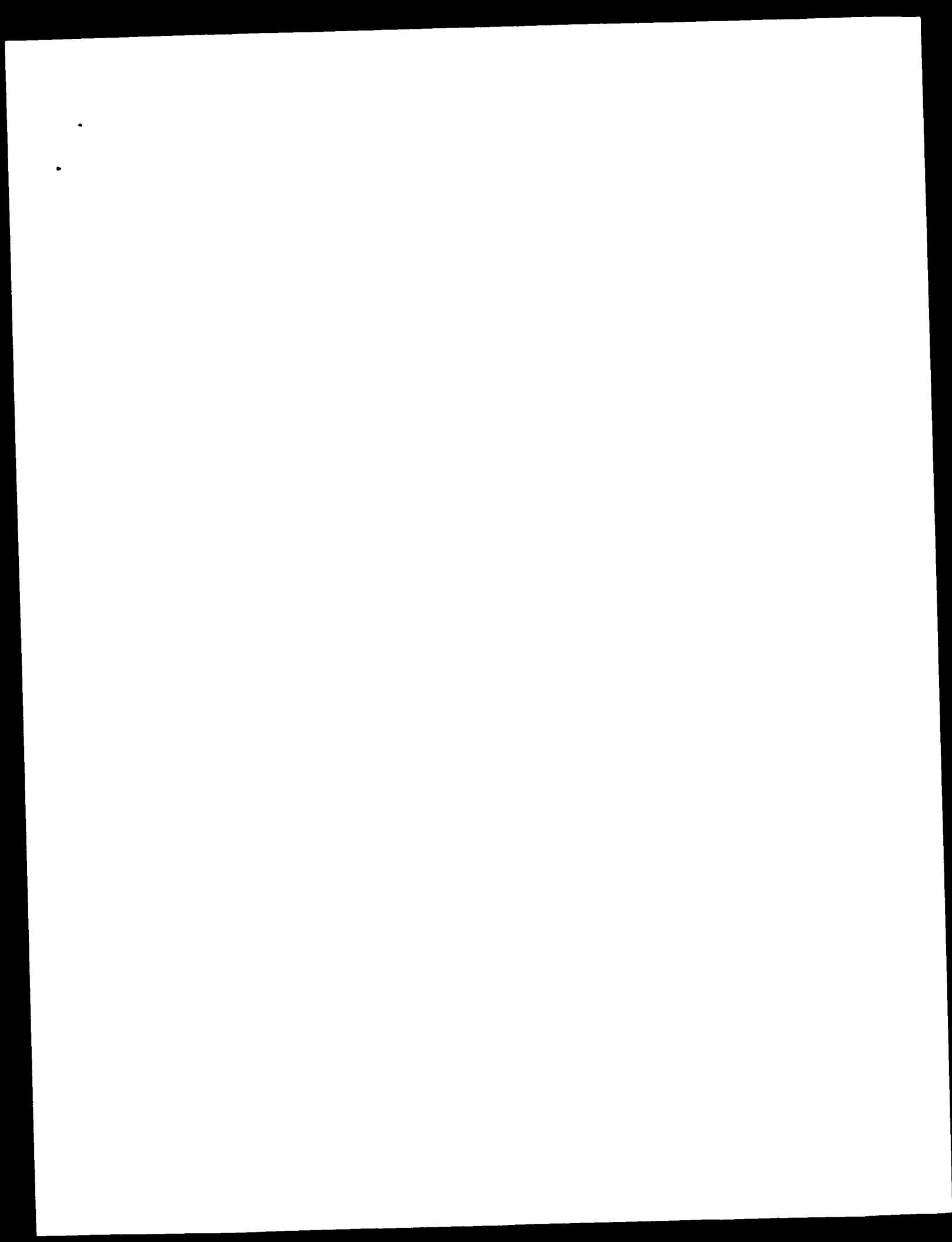
RESULT 75
US-10-183-012-496
Sequence 496, Application US/10183012
Publication No. US2000021056A1
GENERAL INFORMATION
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desrochers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Galswsky, Paul J.
APPLICANT: Gurney, Austin I.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Macanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SEQUENCE AND TRANSMEMBRANE PROPERTIES AND NUMBER
TITLE OF INVENTION: ACTS ENCODING THE SAME
FILE REFERENCE: P43091017 US/01/01/000
CURRENT AFFILIATION NUMBER: 60/054263
PRIORITY FILING DATE: 1997-06-26
PRIORITY APPLICATION REMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 012
SEQ ID NO 496
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapien
US-10-183-012-496


```

: PRIOP APPLICATION NUMBER: 60/080653
Query Match: 2.1%; Score 9; DB 3; Length 458;
Best Local Similarity: 100.0%; Prid No 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 201 GASTOITF 209
    |||||
Db 207 GASTOITF 215

```

Search completed: June 30, 2003, 15:07:13
 Tot time : 31 secs



EARLIER FILING DATE 1999-02-04
 EARLIER APPLICATION NUMBER 09/120,449
 EARLIER FILING DATE 1998-07-24
 EARLIER APPLICATION NUMBER 09/120,449
 EARLIER FILING DATE 1998-07-24
 EARLIER APPLICATION NUMBER 09/120,449
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 5
 LENGTH 428
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-370-265-5

Query March 100 % Score 2250 DB 4 Length 428
 Best Local Similarity 100 % Field NO 206 246
 Matches 428 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 MATWTVTFMVAIVYVAVSARHNNVWEEJIFLSMSPINVASIPIHMEASISG 60
 DE 1 MATWTVTFMVAIVYVAVSARHNNVWEEJIFLSMSPINVASIPIHMEASISG 60
 QY 61 FHVTVFVGMPPGLPILESSEHFSVTFSSATFVGGHQAETVGGILGARSIRSH 120
 DE 61 FHVTVFVGMPPGLPILESSEHFSVTFSSATFVGGHQAETVGGILGARSIRSH 120
 QY 121 KPTTVVATAGPILDEHVAALLFEVKEIFKSPFLVPGSVGIMDSCDEGLAWTV 180
 DE 121 KPTTVVATAGPILDEHVAALLFEVKEIFKSPFLVPGSVGIMDSCDEGLAWTV 180
 QY 161 NEFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGH 240
 DE 161 NEFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGH 240
 QY 241 SYLSPGPAALATLQAFETGTHGTPRACIPOMIAEMIQQSVYVYVYVYVYVYV 300
 DE 241 SYLSPGPAALATLQAFETGTHGTPRACIPOMIAEMIQQSVYVYVYVYVYVYV 300
 QY 301 EPCVAVLVVGRHIFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGH 360
 DE 301 EPCVAVLVVGRHIFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGH 360
 QY 361 EVGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTH 420
 DE 361 EVGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTH 420
 QY 421 LOSUGISH 428
 DE 421 LOSUGISH 428

RESULT 9
 US-09-608-285A-7
 Sequence 7, Application US/09608285A
 Patent No. 6335013
 GENERAL INFORMATION:
 APPLICANT: Ford, John
 APPLICANT: Muleto, Julio
 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE TREATMENT OF INVENTION: POLYMERIZATION
 TITLE OF INVENTION: POLYMERIZATION
 FILE REFERENCE: 29110/31570
 CURRENT APPLICATION NUMBER: US/09/608,285A
 CURRENT FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: 09/583,931
 PRIOR FILING DATE: 2000-05-06
 PRIOR APPLICATION NUMBER: 09/567,400
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/481,225
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: 09/477,167
 PRIOR FILING DATE: 1999-08-06
 PRIOR APPLICATION NUMBER: 09/453,719
 PRIOR FILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: 09/350,836
 PRIOR FILING DATE: 1999-07-13
 PRIOR APPLICATION NUMBER: 09/273,447
 PRIOR FILING DATE: 1999-03-19
 PRIOR APPLICATION NUMBER: 09/244,444
 PRIOR FILING DATE: 1999-04-04
 PRIOR APPLICATION NUMBER: 09/122,449
 PRIOR FILING DATE: 1998-07-24
 PRIOR APPLICATION NUMBER: 09/113,205
 PRIOR FILING DATE: 1998-07-16
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 7
 LENGTH 428
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-608-285A-7

Query March 99.8% Score 2235 DB 4 Length 428
 Best Local Similarity 99.8% Field NO 148 246
 Matches 428 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 MATWTVTFMVAIVYVAVSARHNNVWEEJIFLSMSPINVASIPIHMEASISG 60
 DE 1 MATWTVTFMVAIVYVAVSARHNNVWEEJIFLSMSPINVASIPIHMEASISG 60
 QY 61 FHVTVFVGMPPGLPILESSEHFSVTFSSATFVGGHQAETVGGILGARSIRSH 120
 DE 61 FHVTVFVGMPPGLPILESSEHFSVTFSSATFVGGHQAETVGGILGARSIRSH 120
 QY 121 KPTTVVATAGPILDEHVAALLFEVKEIFKSPFLVPGSVGIMDSCDEGLAWTV 180
 DE 121 KPTTVVATAGPILDEHVAALLFEVKEIFKSPFLVPGSVGIMDSCDEGLAWTV 180
 QY 161 NEFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGH 240
 DE 161 NEFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGH 240
 QY 241 SYLSPGPAALATLQAFETGTHGTPRACIPOMIAEMIQQSVYVYVYVYVYVYV 300
 DE 241 SYLSPGPAALATLQAFETGTHGTPRACIPOMIAEMIQQSVYVYVYVYVYVYV 300
 QY 301 EPCVAVLVVGRHIFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGH 360
 DE 301 EPCVAVLVVGRHIFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGHNRGTFVGGH 360
 QY 361 EVGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTH 420
 DE 361 EVGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTHGTH 420
 QY 421 LOSUGISH 428
 DE 421 LOSUGISH 428

RESULT 10
 US-09-350-836B-7
 Sequence 7, Application US/09350836B
 Patent No. 6281645
 GENERAL INFORMATION:
 APPLICANT: Ford, John
 APPLICANT: Muleto, Julio
 TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE TREATMENT OF INVENTION: POLYMERIZATION
 TITLE OF INVENTION: POLYMERIZATION
 FILE REFERENCE: 29110/31570
 CURRENT APPLICATION NUMBER: US/09/350,836B
 CURRENT FILING DATE: 1999-07-09
 PRIOR APPLICATION NUMBER: 09/273,447
 PRIOR FILING DATE: 1999-03-19
 PRIOR APPLICATION NUMBER: 09/244,444
 PRIOR FILING DATE: 1999-04-04
 PRIOR APPLICATION NUMBER: 09/122,449
 PRIOR FILING DATE: 1998-07-24
 PRIOR APPLICATION NUMBER: 09/113,205
 PRIOR FILING DATE: 1998-07-16

Query Match 100.0% Score 428, DB 23, Length 428;
 Best Local Stability 100.0%, Pct 0.0,
 Matches 428; Conservative 0, Mismatches 0, Indels 0, Gaps 0

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 QY 2 FHTTFFVVF 120
 D 2 FHTTFFVVF 120
 QY 3 FHTTFFVVF 180
 D 3 FHTTFFVVF 180
 QY 4 FHTTFFVVF 240
 D 4 FHTTFFVVF 240
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 D 5 FHTTFFVVF 300
 QY 6 FHTTFFVVF 360
 D 6 FHTTFFVVF 360
 QY 7 FHTTFFVVF 420
 D 7 FHTTFFVVF 420

RESULT 21
 US-09-905-744-6
 Sequence 6 Application US/09090744
 GENERAL INFORMATION:
 APPLICANT: Chadwick, Brian Paul
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD3 INHIBITORS
 TITLE OF INVENTION: POLYMERIZABLE AND NOVEL ACTS
 FILE REFERENCE: 0909-066
 CURRENT APPLICATION NUMBER: 09/090744
 PRIOR APPLICATION NUMBER: 09/240,639
 FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 6
 LENGTH 428
 TYPE: PRN
 ORGANISM: Homo sapiens
 US-09-905-744-6

Query Match 100.0% Score 428, DB 23, Length 428;
 Best Local Stability 100.0%, Pct 0.0,
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 QY 2 FHTTFFVVF 120
 D 2 FHTTFFVVF 120
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 QY 4 FHTTFFVVF 240
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Query Match 100.0% Score 428, DB 23, Length 428;
 Best Local Stability 100.0%, Pct 0.0,
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 D 2 FHTTFFVVF 120
 QY 3 FHTTFFVVF 180
 D 3 FHTTFFVVF 180
 QY 4 FHTTFFVVF 240
 D 4 FHTTFFVVF 240
 QY 5 FHTTFFVVF 300
 D 5 FHTTFFVVF 300
 QY 6 FHTTFFVVF 360
 D 6 FHTTFFVVF 360
 QY 7 FHTTFFVVF 420
 D 7 FHTTFFVVF 420

RESULT 22
 US-09-905-744-9
 Sequence 9 Application US/09090744
 GENERAL INFORMATION:
 APPLICANT: Chadwick, Brian Paul
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD3 INHIBITORS
 TITLE OF INVENTION: POLYMERIZABLE AND NOVEL ACTS
 FILE REFERENCE: 0909-066
 CURRENT APPLICATION NUMBER: 09/090744
 PRIOR APPLICATION NUMBER: 09/240,639
 FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 9
 LENGTH 428
 TYPE: PRN
 ORGANISM: Homo sapiens
 US-09-905-744-9

Query Match 100.0% Score 428, DB 23, Length 428;
 Best Local Stability 100.0%, Pct 0.0,
 Matches 428; Conservative 0, Mismatches 0, Indels 0, Gaps 0

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 QY 4 FHTTFFVVF 240
 D 4 FHTTFFVVF 240
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 QY 6 FHTTFFVVF 360
 D 6 FHTTFFVVF 360
 QY 7 FHTTFFVVF 420
 D 7 FHTTFFVVF 420


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; PRIO# FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 429
; TYPE: CDS
; ORGANISM: Homo sapiens
US-10-091-085-3

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Query Match:	100 %	Coverage:	426 / 426	Identity:	100 %
Best Local Similarity:	100 %	Expect N:	0		
Matches: 428, Conservative:	0	Mismatches:	0	Indels:	0
		Gaps:	0		

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RESULT 26
US-10-091-085-5

[illegible]

US-10-091-085-5

Query Match	100.00%	Score 428	DE 24	1997.11.4.24
Best Local Similarity	100.00% <th>1997.11.4.0</th> <td></td> <td></td>	1997.11.4.0		
Matches 4.6	unsubstituted	0	1997.11.4.24	

[illegible]

US-10-09

Sequence 3, Application US/10092063
; GENERAL INFORMATION:

APPLICANT: Mulero, Giulio
TITLE OF INVENTION: METHOD

FILE OF INVENTION, METHOD AND MATERIAL RELATING TO THE
TITLE REFERENCE: 28110/35928
CURRENT APPLICATION NUMBER: US/59/032,063

CURRENT FILING DATE: 2004-03-05
 PRIOR FILING NUMBER: 07/370,245
 PRIOR FILING DATE: 2003-01-31
 PRIOR APPLICATION NUMBER: PC/C039/1618C
 PRIOR FILING DATE: 1999-07-16
 PRIOR APPLICATION NUMBER: 09/356,846
 PRIOR FILING DATE: 1997-07-30
 PRIOR APPLICATION NUMBER: 09/273,447
 PRIOR FILING DATE: 1997-07-30
 PRIOR APPLICATION NUMBER: 09/271,114
 PRIOR FILING DATE: 1997-02-04
 PRIOR APPLICATION NUMBER: 09/122,449
 PRIOR FILING DATE: 1998-07-24
 PRIOR APPLICATION NUMBER: 09/114,208
 PRIOR FILING DATE: 1998-07-16
 NUMBER OF EFF: 1258, 39
 SOFTWARE: Parentin Ver. 2.0
 SEQ ID NO 3
 LENGTH: 498
 TYPE: PRT
 ORGANISM: Homo sapiens
 OS: 10-092-063-3

Query Match	100.0%	Score 428	DE 24	Length 474
Best local similarity	100.0%	Find. No. 0		

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GenCore Version 5.1.6
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OM Protein - protein search, using sw model

Run on: 2003-06-30 14:43:29, Search time: 11:30:43
(without alignments)

1013 391 Million-cell matches/sec

Title: US-09-905-744B-6
Perfect score: 2250
Sequence: 1 MATSWGTGTFWLVYVTVTA EFWAGVATGTHLQVQVLAHL

Filtering: Filter: EFASTWMT
Gapop: 10.0, Gapext: 0.5

Searches: 1197705 seqs, 2645641 residues

Total number of hits satisfying chosen parameters: 1197705

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

Database: 1 Penting Polystyrene AA Row *

Pred. No. is the number of results produced by the search. A score greater than or equal to the score of the result being filtered, and is derived by analyzing the result being filtered.

SUMMARIES

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45	999	44.4	456	US-09-905-744B-2	Sequence 6050, AP

Query Match 100.0% Score 2250, DB 5, Length 428
 Best Local Similarity 100.0%, Pct 1, No. 1, 100.0%
 Matches 429, Conserved 0, Mismatches 0, Indels 0, Gaps 0

Q 1 MATSWIVTEFMDVAVSASVSHKQCTWFEQIFLSKQCFINVASITQINQDASTGT 60
 E 1 MATSWIVTEFMDVAVSASVSHKQCTWFEQIFLSKQCFINVASITQINQDASTGT 60
 Q 2 PHVAVTEVQMPKSPILPSPVHCVFVLAATPQVQVAFVAVVAVVAVVAVVAVV 120
 D 2 PHVAVTEVQMPKSPILPSPVHCVFVLAATPQVQVAFVAVVAVVAVVAVVAVV 120
 Q 61 RHVAVTEVQMPKSPILPSPVHCVFVLAATPQVQVAFVAVVAVVAVVAVVAVV 120
 D 61 RHVAVTEVQMPKSPILPSPVHCVFVLAATPQVQVAFVAVVAVVAVVAVVAVV 120
 Q 121 KPTPVVATATQPHLPVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 180
 D 121 KPTPVVATATQPHLPVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 180
 Q 141 NPLTQDHPCEVYVITLQVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 240
 D 141 NPLTQDHPCEVYVITLQVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 240
 Q 241 SYLGGVAAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 300
 D 241 SYLGGVAAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 300
 Q 301 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 360
 D 301 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 360
 Q 361 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420
 D 361 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420
 Q 421 LOSLQISH 428
 D 421 LOSLQISH 428

RESULT 10

US-09-905-589A-6
 Sequence 6, Application US/09905589A
 GENERAL INFORMATION
 APPLICANT: Chasick, Brian Paul
 APPLICANT: Fritsch, Anna Maria
 TITLE OF INVENTION: METHOD AND COMPOSITION RELATING TO THE TREATMENT OF
 TITLE OF INVENTION: ACIDS
 FILE REFERENCE: 28110/261200
 CURRENT APPLICATION NUMBER: US/09/905,589A
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: 09/240,639
 PRIOR FILING DATE: 1999-01-26
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: Patent version 3.1
 SEQ ID NO 6
 LENGTH: 428
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-905-589A-6

Query Match 100.0% Score 2250, DB 5, Length 428
 Best Local Similarity 100.0%, Pct 1, No. 1, 100.0%
 Matches 429, Conserved 0, Mismatches 0, Indels 0, Gaps 0

Q 1 MATSWIVTEFMDVAVSASVSHKQCTWFEQIFLSKQCFINVASITQINQDASTGT 60
 D 1 MATSWIVTEFMDVAVSASVSHKQCTWFEQIFLSKQCFINVASITQINQDASTGT 60
 Q 61 RHVAVTEVQMPKSPILPSPVHCVFVLAATPQVQVAFVAVVAVVAVVAVVAVV 120
 D 61 RHVAVTEVQMPKSPILPSPVHCVFVLAATPQVQVAFVAVVAVVAVVAVVAVV 120
 Q 121 KPTPVVATATQPHLPVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 180
 D 121 KPTPVVATATQPHLPVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 180

Q 121 KPTPVVATATQPHLPVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 180
 D 121 KPTPVVATATQPHLPVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 180
 Q 241 SYLGGVAAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 300
 D 241 SYLGGVAAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 300
 Q 301 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 360
 D 301 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 360
 Q 361 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420
 D 361 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420
 Q 421 LOSLQISH 428
 D 421 LOSLQISH 428

RESULT 11

US-09-905-589A-9
 Sequence 9, Application US/09905589A
 GENERAL INFORMATION
 APPLICANT: Chasick, Brian Paul
 APPLICANT: Fritsch, Anna Maria
 TITLE OF INVENTION: METHOD AND COMPOSITION RELATING TO THE TREATMENT OF
 TITLE OF INVENTION: ACIDS
 FILE REFERENCE: 28110/261200
 CURRENT APPLICATION NUMBER: US/09/905,589A
 CURRENT FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: 09/240,639
 PRIOR FILING DATE: 1999-01-26
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: Patent version 3.1
 SEQ ID NO 9
 LENGTH: 428
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-905-589A-9

Query Match 100.0% Score 2250, DB 5, Length 428
 Best Local Similarity 100.0%, Pct 1, No. 1, 100.0%
 Matches 429, Conserved 0, Mismatches 0, Indels 0, Gaps 0

Q 1 MATSWIVTEFMDVAVSASVSHKQCTWFEQIFLSKQCFINVASITQINQDASTGT 60
 D 1 MATSWIVTEFMDVAVSASVSHKQCTWFEQIFLSKQCFINVASITQINQDASTGT 60
 Q 61 RHVAVTEVQMPKSPILPSPVHCVFVLAATPQVQVAFVAVVAVVAVVAVVAVV 120
 D 61 RHVAVTEVQMPKSPILPSPVHCVFVLAATPQVQVAFVAVVAVVAVVAVVAVV 120
 Q 121 KPTPVVATATQPHLPVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 180
 D 121 KPTPVVATATQPHLPVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 180
 Q 241 SYLGGVAAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 300
 D 241 SYLGGVAAVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 300
 Q 301 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 360
 D 301 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 360
 Q 361 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420
 D 361 EPTVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVVAVV 420

Mon Jun 30 15:09:21 2003

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Spool 01 completed: June 30, 2003, 14: 01:52
Jobs: 1000 1 111 10000

GenCore version 5.1.6
CQIY1987 (01 Jan - 2003 Compugen Ltd)

CM protein - protein search, using sw model

Run on: June 30, 2003, 14:14:17 ; Search time 21 seconds
(without alignment)
771,820 Million cells updates/sec

Title: US-09-905-744b-6
Perfect score: 2250
Sequence: 1 MATSWGVTVPMVLVSCVCSA ETCMAL/ATPHILQSLGISH 428

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 110932 seq, 4147329 residues
Total number of hits satisfying chosen parameters: 112992

Minimum DB seq length: 6
Maximum DB seq length: 290700000

Post-processing: Minimum Match 100
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt 35.1
Prod No is the number of results produced by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the data base statistics.

SUMMARIES

Result No.	Score	Match	Length	FP	ID	Description
1	2250	100	428	1	ENPE_HUMAN	000766 hemoglobin
2	1934.6	99.7	428	1	ENPE_MOUSE	000766 hemoglobin
3	1933.6	99.4	428	1	ENPE_MEKAN	000766 hemoglobin
4	290	44.4	484	1	ENPE_HUMAN	000766 hemoglobin
5	582	43.4	456	1	ENPE_FAT	000766 hemoglobin
6	489	21.7	456	1	ENPE_PEA	000766 hemoglobin
7	493.5	21.5	456	1	ENPE_MOUSE	000766 hemoglobin
8	446.5	19.7	456	1	ENPE_MOUSE	000766 hemoglobin
9	387.5	17.7	456	1	ENPE_MOUSE	000766 hemoglobin
10	385	17.1	456	1	ENPE_MOUSE	000766 hemoglobin
11	383	17.0	456	1	ENPE_MOUSE	000766 hemoglobin
12	370	16.6	456	1	ENPE_MOUSE	000766 hemoglobin
13	370	16.4	456	1	ENPE_MOUSE	000766 hemoglobin
14	365	16.2	456	1	ENPE_MOUSE	000766 hemoglobin
15	360.5	16.0	456	1	ENPE_MOUSE	000766 hemoglobin
16	357	15.7	456	1	ENPE_MOUSE	000766 hemoglobin
17	352	15.7	456	1	ENPE_MOUSE	000766 hemoglobin
18	351	15.5	456	1	ENPE_MOUSE	000766 hemoglobin
19	348.5	15.5	456	1	ENPE_MOUSE	000766 hemoglobin
20	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
21	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
22	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
23	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
24	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
25	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
26	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
27	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
28	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
29	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
30	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
31	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
32	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin
33	348.5	15.4	456	1	ENPE_MOUSE	000766 hemoglobin

ALIGNMENTS

RESULT 1	ID	ENPE_HUMAN	STANDARD	PRT	428 AA	DESCRIPTION
AC	075356	ENPE_HUMAN	STANDARD	PRT	428 AA	000766 hemoglobin
AT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
CT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
DT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
ET	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
FT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
GT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
HT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
IT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
JT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
KT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
LT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
MT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
NT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
OT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
PT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
QT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
RT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
ST	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
TT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
UT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
VT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
WT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
XT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
YT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
ZT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
AT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
BT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
CT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
DT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
ET	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
FT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
GT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
HT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
IT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
JT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
KT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
LT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
MT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
NT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
OT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
PT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
QT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
RT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
ST	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
TT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
UT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
VT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
WT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
XT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
YT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin
ZT	16-OCT-2001	(Ref. 40, last sequence update)				000766 hemoglobin

[illegible][illegible]

[illegible][illegible]

DE EMBL; AF465240; AAL69974.1; -.
 DE InterPro; IPR000487; G0A1_G0A1_NTPase
 DE Pfam; PF01150; GDA1_CD39.1.
 DE ProSITE, Pro1249; CAT_2121; NTPASE_1
 SU SEQUENCE 556 AA; 61588 MW; 1D911E3D6A8B8B85 Ck; 64;

Query Match	23.9%	Score 538.5	DB 3	Length 566
Best Local	Score 741.7	Prd 0.2076		
Matches	144	Conservative	61	Mismatches 157
				Indels 57
				Gaps 13

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Q4 4 YIMTJASTJGPHVTFVWAMPJPHLESEVTSVPHJ SAEVOPKQZAVJGTL 108
D4 134 YVMTJASTJGPHVTFVWAMPJPHLESEVTSVPHJ SAEVOPKQZAVJGTL 191
Q5 109 EAVFTSIPSHWITPVVLLATAPLLEPHVAPLLEVPJEPKZ PFTVPOKSNM 167
D5 134 EAVFTSIPSHWITPVVLLATAPLLEPHVAPLLEVPJEPKZ PFTVPOKSNM 251
Q6 168 EESTREIIAMVNTLITLHSH PLEVTJLITLJGASVITFLQPEKYLECPHRS 223
D6 252 EESTREIIAMVNTLITLHSH PLEVTJLITLJGASVITFLQPEKYLECPHRS 311
Q7 224 YTSREPRJGTLITRGOCPJPAEL.....ALAEPEPEPEPEPEPEPE 279
D7 312 YTSREPRJGTLITRGOCPJPAEL.....ALAEPEPEPEPEPEPEPE 368
Q8 279 L.....PFWFAEFTFVJYVYVYVNEVEVEVEVEVEVEVEVEVEVE 329
D8 368 L.....PFWFAEFTFVJYVYVYVNEVEVEVEVEVEVEVEVEVEVE 423
Q9 319 EEXPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE 374
D9 423 EEXPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE 483
Q0 364 ENEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE 421
D0 484 ENEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPEPE 541

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RESULT 8
Q1TGH6
ID QATGH6
FEEWIMJHAWY,
EET, 22 MAY.

[illegible]

G4 GDAL
Candida albicans (Yeast),
OS
Eukaryota, Fungi, Ascomycota, Basidiomycota,
C
Saccharomycotina, Microsporidia, Chytridiomycota,
COP
Fungi Maxilicetia

R1 [1]
R2 SEQUENCE FROM M.A.
R3
R4 Herrero A B ;
R5
R6 "The Goli: Affine of the Foreign Intelligentsia and Affairs
R7 morphological characterisation and cultural interaction "
R8

P3 Submitted: 08/07/2013 09:31 EMBL/GenBank/CCDC Data Accession:
D3 EMBL: A0421721; CAD18370.1; --
P4 Hydrated
SEQUENCE 599 AA; 65922 MW; EEE7AAFEFEEB4EA DPTG4;

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Query Match: 32.0% Score: 117.0, Gap: 0, Length: 500;
Best Local Similarity: 32.0% Start: 50, End: 146;
Matches: 143; Conservative: 65; Mismatches: 148; Indels: 83; Gaps: 15;

QY 49 YGIMPLASTSTRIRIVTFFVAMPQKPLIRSEKTSVTFSAFVLEFAAEVWML 104
DE 163 IVIMIASTSPRVVITNTQV--PFLIESEEESEEESEEESEEEVYQVQSEIEL 220
CY 109 EVAKQSPFGRHMTITVPAIASPEERHAPAEVEVEFEK--VF--TIRNDSYK 166
CH 221 EVMLKPVYDPSKCFVAVPTACHILDEKSALEIEEHLIEVYFAVQENQSL 280

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[illegible]

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PROGRAM 3
      Q9HEM6
      AC Q9HEM6;
      END;

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DT 01-MAR-2001 (Tremblay, 16, Last sequence updated)
 DE 01-FEB-2001 (Tremblay, 15, Last annotation update)
 DE Guanosine diphosphatase.
 GN GDA1.

[illegible][illegible]

[illegible][illegible]

Genome version 5.1.6
Copyright (c) 1993 - 2003 Cytogen Inc.

OK protein - protein search, using sw-mag-1

Run on: June 30, 2003, 14:50:53, Search time 53.34016s

(without alignments)
902 478 Million cells updated/seq

Title: US-09-905-744B 6

Perfect score: 2250

Sequence: 1 MATSWGVFPMVAVSCVCSAFTWNAIGATHTLISRTISQ 428

Scoring table:

PROSCW62
Gapop 10.0, Gapext 0.5

Searched: 42469 seqs, 10947822 positions 439000

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 6

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications_AA:
1: /cgn2-6/prodata/2/pubpa/US09_NEW_PUB pep:
2: /cgn2-6/prodata/2/pubpa/PCR_NEW_PUB pep:
3: /cgn2-6/prodata/2/pubpa/US06_NEW_PUB pep:
4: /cgn2-6/prodata/2/pubpa/US06_NEW_PUB pep:
5: /cgn2-6/prodata/2/pubpa/US07_NEW_PUB pep:
6: /cgn2-6/prodata/2/pubpa/US07_NEW_PUB pep:
7: /cgn2-6/prodata/2/pubpa/US07_NEW_PUB pep:
8: /cgn2-6/prodata/2/pubpa/US07_NEW_PUB pep:
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13: /cgn2-6/prodata/2/pubpa/US07_NEW_PUB pep:
14: /cgn2-6/prodata/2/pubpa/US07_NEW_PUB pep:

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	2250	100%	428	US-10-092-063-3	Sequence 1, APT1
2	2250	100%	428	US-10-092-063-3	Sequence 2, APT1
3	2250	100%	428	US-10-092-063-3	Sequence 3, APT1
4	2250	100%	428	US-10-092-063-3	Sequence 4, APT1
5	2235	99%	428	US-10-092-063-3	Sequence 5, APT1
6	2235	99%	428	US-10-092-063-3	Sequence 6, APT1
7	2194	94%	428	US-10-092-063-3	Sequence 7, APT1
8	1837.5	81.7	465	US-10-092-063-3	Sequence 8, APT1
9	1660	73.8	320	US-09-925-269-876	Sequence 876, APT
10	1660	73.8	320	US-09-925-269-876	Sequence 876, APT
11	999	44%	428	US-10-092-063-3	Sequence 9, APT1
12	590	24%	428	US-09-847-147-4	Sequence 1, APT1
13	533	23%	428	US-09-847-147-4	Sequence 2, APT1
14	507.5	22%	428	US-09-129-112-9	Sequence 3, APT1
15	503.5	22%	428	US-09-129-112-9	Sequence 4, APT1
16	498	22%	428	US-09-129-112-9	Sequence 5, APT1
17	491.5	21.8	428	US-09-129-112-9	Sequence 6, APT1
18	367	16%	428	US-09-847-147-4	Sequence 1, APT1
19	368.5	15%	428	US-10-176-752-496	Sequence 496, APT

20	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
21	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
22	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
23	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
24	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
25	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
26	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
27	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
28	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
29	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
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32	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
33	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
34	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
35	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
36	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
37	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
38	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
39	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
40	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
41	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
42	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
43	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
44	368.5	15%	428	US-10-176-752-496	Sequence 496, APT
45	368.5	15%	428	US-10-176-752-496	Sequence 496, APT

ALIGNMENTS

RESULT 1
US-10-092-063-3
Sequence 1, APT1
Query Match: 100%, Length: 428
Post-local similarity: 100%, E: 1.0e-205
Matches: 428, Mismatches: 0, Indels: 0
1 MATSWGVFPMVAVSCVCSAFTWNAIGATHTLISRTISQ 428
MATSWGVFPMVAVSCVCSAFTWNAIGATHTLISRTISQ 428
US-10-092-063-3

Query Match: 100%, Length: 428
Post-local similarity: 100%, E: 1.0e-205
Matches: 428, Mismatches: 0, Indels: 0
1 MATSWGVFPMVAVSCVCSAFTWNAIGATHTLISRTISQ 428
MATSWGVFPMVAVSCVCSAFTWNAIGATHTLISRTISQ 428
US-10-092-063-3

09	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	
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Patent No. US 2002/0094677 A1
GENERAL INFORMATION:
APPLICANT: Ford, John
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO N-VELT
TITLE OF INVENTION: POLYHYDRIES
FILE REFERENCE: 2010/035661
CURRENT APPLICATION NUMBER: 05/10/091,045
CURRENT FILING DATE: 2002-01-05
PRIOR APPLICATION NUMBER: 04/100,846
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 09/273,447
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: 09/118,706
PRIOR FILING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/100,449
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: 09/444,444
PRIOR FILING DATE: 1999-02-04
NUMBER OF SEQ. ID NOS: 24
SOFTWARE: Patent to Vol. 1.1
SEQ. ID NO. 1
LENGTH: 428
TYPE: PPT
ORGANISM: Homo sapiens
TSS: 10 091 045 3
Query Match: 100.0% Score: 2950.19, 428 100.0% 4.34
Best Local Similarity: 100.0% Prod. No. 1, 000, 000
Matches: 428; Conservative: 0; Mismatch: 0; Gaps: 0

[illegible]

GenCode Version 2.1
 09/10/1997 10:19:21 2003 2003 2003 2003

at protein - protein search, using sw model

Run on: Sun Jun 29 2003 14:46:17, Search time: 47 seconds
 (without alignments)
 875,437 Million cell updates/sec

Title: US-09-905-744b-6

Perfect score: 2250

Sequence: 1 MATSWIVFEMIVSWVCSA

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Search: 283224 seqs, 96124422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database: 1: D111*
 2: D112*
 3: D113*
 4: D114*

Prod M is the sum of results of individual hits. A score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No	Score	Match	Length	DB ID	Description
1	616.5	37.4	479	T23508	hypothetical protein
2	598.5	37.4	479	T23508	hypothetical protein
3	489	37.4	479	T23508	hypothetical protein
4	483.5	37.4	479	T23508	hypothetical protein
5	446.5	37.4	479	T23508	hypothetical protein
6	425.5	37.4	479	T23508	hypothetical protein
7	387.5	37.4	479	T23508	hypothetical protein
8	372.5	37.4	479	T23508	hypothetical protein
9	372.5	37.4	479	T23508	hypothetical protein
10	372.5	37.4	479	T23508	hypothetical protein
11	351	37.4	479	T23508	hypothetical protein
12	347	37.4	479	T23508	hypothetical protein
13	329.5	37.4	479	T23508	hypothetical protein
14	324	37.4	479	T23508	hypothetical protein
15	318	37.4	479	T23508	hypothetical protein
16	318	37.4	479	T23508	hypothetical protein
17	318	37.4	479	T23508	hypothetical protein
18	318	37.4	479	T23508	hypothetical protein
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28	318	37.4	479	T23508	hypothetical protein
29	318	37.4	479	T23508	hypothetical protein
30	318	37.4	479	T23508	hypothetical protein

30	96	4.3	711	2	566749	hypothetical protein
31	96	4.3	711	2	566749	hypothetical protein
32	96	4.3	711	2	566749	hypothetical protein
33	96	4.3	711	2	566749	hypothetical protein
34	96	4.3	711	2	566749	hypothetical protein
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36	96	4.3	711	2	566749	hypothetical protein
37	96	4.3	711	2	566749	hypothetical protein
38	96	4.3	711	2	566749	hypothetical protein
39	96	4.3	711	2	566749	hypothetical protein
40	96	4.3	711	2	566749	hypothetical protein
41	96	4.3	711	2	566749	hypothetical protein
42	96	4.3	711	2	566749	hypothetical protein
43	96	4.3	711	2	566749	hypothetical protein
44	96	4.3	711	2	566749	hypothetical protein
45	96	4.3	711	2	566749	hypothetical protein

ALIGNMENTS

RESULT 1

T23508

hypothetical protein K0810.4 - Caenorhabditis elegans

Species: Caenorhabditis elegans

Accession: T23508

Submitted to the EMBL Data Library, November 1996

Accession number: Z13750

Accession: T23508

Accession: T23508

Accession: T23508

Accession: T23508

Accession: T23508

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Accession: T23508

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Accession: T23508

30	96	4.3	711	2	566749	hypothetical protein
31	96	4.3	711	2	566749	hypothetical protein
32	96	4.3	711	2	566749	hypothetical protein
33	96	4.3	711	2	566749	hypothetical protein
34	96	4.3	711	2	566749	hypothetical protein
35	96	4.3	711	2	566749	hypothetical protein
36	96	4.3	711	2	566749	hypothetical protein
37	96	4.3	711	2	566749	hypothetical protein
38	96	4.3	711	2	566749	hypothetical protein
39	96	4.3	711	2	566749	hypothetical protein
40	96	4.3	711	2	566749	hypothetical protein
41	96	4.3	711	2	566749	hypothetical protein
42	96	4.3	711	2	566749	hypothetical protein
43	96	4.3	711	2	566749	hypothetical protein
44	96	4.3	711	2	566749	hypothetical protein
45	96	4.3	711	2	566749	hypothetical protein

ALIGNMENT

1 PROJECT :
 2 US-09-905-744b-6
 3 REPORT NO. :
 4 GENERAL INFORMATION :
 5 APPLICANT :
 6 APPLICANT :
 7 APPLICANT :
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 96 APPLICANT :
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 98 APPLICANT :
 99 APPLICANT :
 100 APPLICANT :

1 PROJECT :
 2 US-09-905-744b-6
 3 REPORT NO. :
 4 GENERAL INFORMATION :
 5 APPLICANT :
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 100 APPLICANT :

PRIOR APPLICATION NUMBER: US 09/091,026
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent In Viro 4.0
SEQ ID NO: 1
LENGTH: 467
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US 09 173 51A 14

Query Match: 1.032 Score: 72 DB: 42 Length: 467
Post Local Similarity: 10.081 Prod. No.: 10062
Matches: 72 Conservative: 07 Mismatches: 07 Indels: 07 Gaps: 07

SV: 54 FILED: 00
11 11 11
db: 61 FILED: 07

RESULT 41
US 09 173 51A 14
Sequence: 14, Application: US/0917351A
Patent No.: 6326472
GENERAL INFORMATION:
APPLICANT: Timms, Theodore R.
APPLICANT: Robert, Johannes Edward Maria
APPLICANT: Antonius
APPLICANT: Samu, Theodore R.
APPLICANT: Bazar, Y. Fernando
APPLICANT: Karelidin, Robert A.
TITLE OF INVENTION: Human Recombinant Proteins, Polypeptides and Methods
NUMBER OF SEQUENCES: 46
RESIDUENT ADDRESS:
ADDRESS: 1045 Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304 1104
TELEPHONE: 650 496 1104
FAX: 650 496 1104
COMPUTER: IBM PC compatible
SOFTWARE: Patent In Viro 4.0, Version: #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/173,51A
FILING DATE: 14 OCT 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 67/066,776
FILING DATE: 17 NOV 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/074,008
FILING DATE: 12 MAR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/081,884
FILING DATE: 15 APR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/096,997
FILING DATE: 10 AUG 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/099,416
FILING DATE: 19 MAR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/104,416
FILING DATE: 19 MAR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/104,416
FILING DATE: 19 MAR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/104,416
FILING DATE: 19 MAR 1998
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Edgar P.
REGISTRATION NUMBER: 44,592
REFERENCE/KEY NUMBER: EX-787X
TELEPHONE: 650 952 9196
TELEFAX: 650 496 1104
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 632 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US 09 173 51A 14

Query Match: 1.032 Score: 72 DB: 42 Length: 632
Post Local Similarity: 10.081 Prod. No.: 10062
Matches: 72 Conservative: 07 Mismatches: 07 Indels: 07 Gaps: 07

SV: 144 FILED: 140
11 11 11
db: 121 FILED: 122

RESULT 42
US 09 173 51A 14
Sequence: 16, Application: US/0917351A
Patent No.: 6326472
GENERAL INFORMATION:
APPLICANT: Timms, Theodore R.
APPLICANT: Robert, Johannes Edward Maria
APPLICANT: Antonius
APPLICANT: Samu, Theodore R.
APPLICANT: Bazar, Y. Fernando
APPLICANT: Karelidin, Robert A.
TITLE OF INVENTION: Human Recombinant Proteins, Polypeptides and Methods
NUMBER OF SEQUENCES: 46
RESIDUENT ADDRESS:
ADDRESS: 1045 Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304 1104
TELEPHONE: 650 496 1104
FAX: 650 496 1104
COMPUTER: IBM PC compatible
SOFTWARE: Patent In Viro 4.0, Version: #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0917351A
FILING DATE: 14 OCT 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 67/066,776
FILING DATE: 17 NOV 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/074,008
FILING DATE: 12 MAR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/081,884
FILING DATE: 15 APR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/096,997
FILING DATE: 10 AUG 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/099,416
FILING DATE: 19 MAR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/104,416
FILING DATE: 19 MAR 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66/104,416
FILING DATE: 19 MAR 1998
ATTORNEY/AGENT INFORMATION:
NAME: Chao, Edgar P.
REGISTRATION NUMBER: 44,592
REFERENCE/KEY NUMBER: EX-787X
TELEPHONE: 650 952 9196
TELEFAX: 650 496 1104
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 614 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-171-151A-16
Query Match: 1.63, Score 71, E-41, Length 614
Best Local Similarity: 100.0%, Posed No. 126,023

Matches: 7, Conservation: 0, Mismatches: 0, Indels: 0, Gaps: 0

Q 134 PILEUP 140
D 106 PILEUP 201

RESULT 33
US-09-198-590-19
Sequence 18, Application US/0919892
Patent No. 5834410

GENERAL INFORMATION:

APPLICANT: Tjian, Robert

APPLICANT: Comai, Lucio

APPLICANT: Dynlacht, Brian D.

APPLICANT: Hoey, Timothy

APPLICANT: Ruffell, Steven

APPLICANT: Tusch, Mark

APPLICANT: Wang, Edith

APPLICANT: Weinberg, Robert G.

TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAGS AND METHODS OF USE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSER: FLEURY, HUBERT, TEST, ALBERT & HUBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-4197

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/198,592

FILING DATE: 28-JAN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Osmun, Richard A

REGISTRATION NUMBER: 36,627

REFERENCE/COCKET NUMBER: A 36650-2/A/AT/PAO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 915122

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-198-582-18

Query Match: 1.63, Score 71, E-41, Length 704
Best Local Similarity: 100.0%, Posed No. 126,023

Matches: 7, Conservation: 0, Mismatches: 0, Indels: 0, Gaps: 0

Q 392 STACTV 398
D 392 GFADSTV 398

RESULT 34

US-09-646-715-18
Sequence 19, Application US/09646715
Patent No. 5837686

GENERAL INFORMATION:

APPLICANT: Tjian, Robert

APPLICANT: Comai, Lucio

APPLICANT: Dynlacht, Brian D.

APPLICANT: Hoey, Timothy

APPLICANT: Ruffell, Steven

APPLICANT: Tusch, Mark

APPLICANT: Wang, Edith

APPLICANT: Weinberg, Robert G.

TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAGS AND METHODS OF USE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSER: FLEURY, HUBERT, TEST, ALBERT & HUBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-4197

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/198,592

FILING DATE: 28-JAN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Osmun, Richard A

REGISTRATION NUMBER: 36,627

REFERENCE/COCKET NUMBER: A 36650-2/A/AT/PAO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 915122

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-646-715-18

Query Match: 1.63, Score 71, E-41, Length 704
Best Local Similarity: 100.0%, Posed No. 126,023

Matches: 7, Conservation: 0, Mismatches: 0, Indels: 0, Gaps: 0

Q 392 STACTV 398
D 392 GFADSTV 398

RESULT 35

US-09-640-406-4
Sequence 4, Application US/09644064
Patent No. 5837638

GENERAL INFORMATION:

APPLICANT: Tjian, Robert

APPLICANT: Comai, Lucio

APPLICANT: Dynlacht, Brian D.

APPLICANT: Hoey, Timothy

APPLICANT: Ruffell, Steven

APPLICANT: Tusch, Mark

APPLICANT: Wang, Edith

APPLICANT: Weinberg, Robert G.

TITLE OF INVENTION: DATA BINDING PROTEIN ASSOCIATED FACTORS

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAGS AND METHODS OF USE

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSER: FLEURY, HUBERT, TEST, ALBERT & HUBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-4197

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/198,592

FILING DATE: 28-JAN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Osmun, Richard A

REGISTRATION NUMBER: 36,627

REFERENCE/COCKET NUMBER: A 36650-2/A/AT/PAO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 915122

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 704 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-646-715-18

Query Match: 1.63, Score 71, E-41, Length 704
Best Local Similarity: 100.0%, Posed No. 126,023

Matches: 7, Conservation: 0, Mismatches: 0, Indels: 0, Gaps: 0

Q 392 STACTV 398
D 392 GFADSTV 398

RESULT 35


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1 GENERAL INFORMATION
2 APPLICANT: SCOTT, MATTHEW P
3 GILBERT, MICHAEL
4 TITLE OF INVENTION: Patched Genes and their use
5 NUMBER OF SEQUENCES: 1
6 REFERENCE TO OTHER
7 ADDRESSER: FISH, MICHAEL, JR., ATTORNEY & COUNSELOR
8 STREET: Four Embarcadero Center, Suite 4100
9 CITY: San Francisco
10 STATE: CA
11 COUNTRY: US
12 ZIP: 94111
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: DOS/MS-DOS
18 SOFTWARE: Patent Release #10, Version #1.0
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: 08/032,768
22 FILING DATE: 02 Aug 1997
23 CLASSIFICATION: C12N
24
25 PRIORITY APPLICATION DATA:
26 APPLICATION NUMBER: 08/056,093
27 FILING DATE: unknown
28 APPLICATION NUMBER: 08/040,404
29 FILING DATE: unknown
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Rowland, Bernard I
32 REGISTRATION NUMBER: 20016
33 PREFERRED LANGUAGE: English
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 415-781-1989
36 TELEFAX: 415-392-3543
37
38 INFORMATION FOR SEQ ID NO. 4:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 1311 amino acids
41 TYPE: amino acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 MOLECULE TYPE: protein
45 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
46
47 US-08-918-659-4
48
49 Query Match 1 68 Score 7, E 4, Length 1311
50 Best Match: similarity 1, sim 100, pos 1, 1311
51 Matches: 7, Conservation of residues: 0, Total: 0, Gap: 0
52
53 179 SPG11A 176
54 |||||
55 a03 SPG11A a03
56
57 RESULT 39
58 PRT-US95-13233-4
59 Sequence 4: Application polynucleotide
60 GENERAL INFORMATION:
61 APPLICANT: THE BOARD OF TRUSTEES OF THE JACOBSON FOUNDATION
62 TITLE OF INVENTION: For and uses and their use
63 NUMBER OF SEQUENCES: 1
64 CORRESPONDENCE ADDRESS:
65 ADDRESSER: Fish, Michael, Jr., Attorney & Counselor
66 STREET: Four Embarcadero Center, Suite 4100
67 CITY: San Francisco
68 STATE: CA
69 COUNTRY: US
70 ZIP: 94111
71
72 COMPUTER READABLE FORM:
73 MEDIUM TYPE: floppy disk
74 COMPUTER: IBM PC compatible
75 OPERATING SYSTEM: DOS/MS-DOS
76 SOFTWARE: Patent Release #10, Version #1.0
77
78 CURRENT APPLICATION DATA:
79 APPLICATION NUMBER: 08/032,768
80 FILING DATE: 02 Aug 1997
81 CLASSIFICATION: C12N
82
83 PRIORITY APPLICATION DATA:
84 APPLICATION NUMBER: 08/056,093
85 FILING DATE: unknown
86 APPLICATION NUMBER: 08/040,404
87 FILING DATE: unknown
88 ATTORNEY/AGENT INFORMATION:
89 NAME: Rowland, Bernard I
90 REGISTRATION NUMBER: 20016
91 PREFERRED LANGUAGE: English
92 TELECOMMUNICATION INFORMATION:
93 TELEPHONE: 415-781-1989
94 TELEFAX: 415-392-3543
95
96 INFORMATION FOR SEQ ID NO. 4:
97 SEQUENCE CHARACTERISTICS:
98 LENGTH: 1311 amino acids
99 TYPE: amino acid
100 STRANDEDNESS: single
101 TOPOLOGY: linear
102 MOLECULE TYPE: protein
103 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
104
105 US-08-918-659-4

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1  ATTENTION NUMBER 157-0395/1223
2  FILING DATE: 06-OCT-1990
3  CLASSIFICATION:
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Rowland, Patricia I
6  REGISTRATION NUMBER: 20015
7  REFERENCE FILE NUMBER: 4-030-1
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 415-781-1863
10 TELEFAX: 415-398-3249
11 INFORMATION FOR SEQ ID NO: 1:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 1311 amino acids
14 TYPE: amino acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: protein
18 PRT US95 12233-4
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1 M. LEBRON, 1718 N. 11th St.
2 1000 1000 1000 1000

3 Query Match 1000 1000 1000 1000
4 Post Local Availability 1000 1000 1000 1000
5 Match 1000 1000 1000 1000

6 Y 1000 1000 1000 1000
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8 RESULT 1000

9 1000 1000 1000 1000

10 1000 1000 1000 1000

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Query Match 1.48, Score 6, DP 4, Length 27,
Best Local Similarity 100.0%, Prod No 72,
Matches 6, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 42 WWSACT 47
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DB 8 WWSACT 13

RESULT 44

US-07-668-648-12
Sequence 12, Application US/0668648
Patent No. 5416192

GENERAL INFORMATION

APPLICANT: Shoyab, Mohamed
APPLICANT: Fawaz, Gregory T
TITLE OF INVENTION: ENZYMINES: NOVEL CYSTEINE RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS

ADDRESSEE: Pennie & Edwards
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036
FILING DATE: 19910819

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fawaz, Gregory T
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0668648
FILING DATE: 19910819

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741

INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: Protein

US-07-668-648-12

Query Match 1.48, Score 6, DP 4, Length 27,
Best Local Similarity 100.0%, Prod No 72,
Matches 6, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 132 GRLUP 137
|||||
DB 5 GRLUP 10

RESULT 45

US-08-429-998-12
Sequence 12, Application US/0842998
Patent No. 5883641

GENERAL INFORMATION

APPLICANT: Shoyab, Mohamed
APPLICANT: Fawaz, Gregory T
TITLE OF INVENTION: ENZYMINES: NOVEL CYSTEINE RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS

ADDRESSEE: Pennie & Edwards
STREET: 1155 Avenue of the Americas
CITY: New York

CITY: New York
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0842998
FILING DATE: 27-Apr-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07668648
FILING DATE: 1991MAR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741
TELEFAX: (212) 869-9741

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: Protein

US-08-429-998-12

Query Match 1.48, Score 6, DP 4, Length 27,
Best Local Similarity 100.0%, Prod No 72,
Matches 6, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 132 GRLUP 137
|||||
DB 5 GRLUP 10

RESULT 46

US-08-429-998-12
Sequence 12, Application US/0842998
Patent No. 5883641

GENERAL INFORMATION

APPLICANT: Shoyab, Mohamed
APPLICANT: Fawaz, Gregory T
TITLE OF INVENTION: ENZYMINES: NOVEL CYSTEINE RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS

ADDRESSEE: Pennie & Edwards
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0842998
FILING DATE: 27-Apr-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07668648
FILING DATE: 1991MAR-1991

ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624 161 999
TELECOMMUNICATION INFORMATION:

[illegible]

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Figure 1. The effect of the concentration of the monomer on the polymerization of α -methylstyrene initiated by BuLi in THF at -78°C . The concentration of the initiator was 0.01 mol/L . The polymerization was terminated by the addition of methanol. The polymerization was carried out in a dry nitrogen atmosphere. The polymerization was carried out in a dry nitrogen atmosphere. The polymerization was carried out in a dry nitrogen atmosphere.

APPELLANT: *Sherry, Michael*
APPELLANT: *Forster, Gregory E.*
APPELLANT: *Forster, Gregory E.*
APPELLANT: *Forster, Gregory E.*

[illegible]

CITY: BOULDER
STATE: WASHINGTON
COUNTY: COA

101-1025 NEW AVALON BLVD
 MONTROSE, N.Y. 11404
 *MONTROSE: 46M 1-11, 11-12, 11-13

PRESENT ADDRESS: P. 771604, 700, 321
ALPHEIATTIN, MINOCHI

NAME: Edward J. McLaughlin

JOHN HENNING ZITTE, INCORPORATED
 TELEPHONE: (703) 528-4000
 FORT LAUDERDALE, FLORIDA 33301

THE UNIVERSITY OF CHICAGO
LIBRARY

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration was adjusted to 1.0 × 10⁸ cells/ml. The cell suspension was mixed with the plant tissue and incubated for 24 h at 28 °C. The plant tissue was then cultured on the selective medium. The transformation efficiency was determined as the number of transformants per 100 mg of plant tissue. The data are the mean ± SD of three independent experiments.

[illegible][illegible]

1. APPLICANT: Robert N. Williams
 2. ADDRESS: 1000 N. 10th Street, Room 100
 3. TITLE OF INVENTION: Method of and means for
 4. TITLE OF INVENTION: protecting a male street
 5. NUMBER OF SHEETS: 1
 6. CORRESPONDENT'S ADDRESS:
 7. ADDRESS: 1000 N. 10th Street, Room 100

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

COUNTRY: United States of America
 EXP: 07/2004

[illegible]

ADDITIONAL INFORMATION: YES NO
EFFECT DATE:

ADDITIONAL INFORMATION: The authors are grateful to the National Science Foundation for support of this work.

RESEARCH AND DEVELOPMENT

PERSONNEL: 600 PERSONS

TECHNOLOGY INFORMATION:

TELETYPE: 100-3446
 INFORMATION: 100-3446
 SECURITY: 100-3446

1. The first step is to identify the problem or question that needs to be addressed. This involves understanding the context and the specific requirements of the task.

[illegible][illegible][illegible][illegible]

GENERAL INFORMATION:
 ADDRESS: 1400 W. Woodward, Oklahoma City, Oklahoma 73106
 APPLICATION: Oklahoma Bureau of Motor Vehicle Title and Registration
 10-10-77

[illegible]

Author	Year	Country	Sample Size	Study Design	Findings
Wong et al.	2001	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2002	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2003	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2004	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2005	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2006	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2007	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2008	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2009	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2010	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2011	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2012	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2013	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2014	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2015	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2016	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2017	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2018	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2019	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2020	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2021	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2022	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2023	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2024	China	1,000	Case-control	Increased risk of lung cancer in smokers
Wong et al.	2025	China	1,000	Case-control	Increased risk of lung cancer in smokers

[illegible]

TYPE: amino acid
 SEQUENCE: amino acid
 TOPIC: amino acid
 MOLECULE TYPE: amino acid
 IN NO 176 500 5

Query Match 1.44 Score 67.76 Length 392
 Best Local Similarity 100.00 Prod. No. 992
 Matched 67.76 of 100.00 of Mismatches 02 Indels 02 Gaps 02

QY 88 PBLAF 34
 DB 19 PBLAF 34

RESULT 54
 IN 08 471 902A 5
 SEQUENCE 5, Application 108/4471902A
 Patent No. 5646744

GENERAL INFORMATION:
 APPLICANT: Foy, B. K.
 TITLE OF INVENTION: Polarity of amino acid
 NUMBER OF SEQUENCES: 16
 CORRESPONDENT ADDRESS:
 ADDRESS: Pennix & Edwards
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036 2711

COMPUTER: IBM PC compatible
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent in Release #10, Version #1.06
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 108/4471902A
 FILING DATE: 06 JUN 1995
 CLASSIFICATION: 540
 ATTORNEY/AGENT INFORMATION:
 NAME: Misko, S. Joseph
 REGISTRATION NUMBER: 18,872
 REFERENCE/AGENT NUMBER: 1101 179
 TELEPHONE: 212 790 1030
 TELEFAX: 212 790 1030
 TELETYPE: 212 790 1030
 TELEFAX: 212 790 1030
 TELETYPE: 212 790 1030

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ 1: 16
 SEQUENCE INFORMATION:
 LENGTH: 39 amino acid
 TYPE: amino acid
 STRANDEDNESS: single
 TOPIC: amino acid
 MOLECULE TYPE: amino acid
 IN 08 471 902A 5

Query Match 1.44 Score 67.76 Length 392
 Best Local Similarity 100.00 Prod. No. 992
 Matched 67.76 of 100.00 of Mismatches 02 Indels 02 Gaps 02

QY 88 PBLAF 34
 DB 19 PBLAF 34

RESULT 54
 IN 08 189 341 5
 SEQUENCE 5, Application 108/4189341

Patent No. 547344
 GENERAL INFORMATION:
 APPLICANT: Foy, B. K.
 ADDRESS: Pennix & Edwards, Inc.

TITLE OF INVENTION: Polarity of amino acid
 NUMBER OF SEQUENCES: 16
 CORRESPONDENT ADDRESS:
 ADDRESS: Pennix & Edwards
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036 2711

COMPUTER: IBM PC compatible
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent in Release #10, Version #1.06
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 108/4189341
 FILING DATE: 06 JUN 1995
 CLASSIFICATION: 540
 ATTORNEY/AGENT INFORMATION:
 NAME: Misko, S. Joseph
 REGISTRATION NUMBER: 18,872
 REFERENCE/AGENT NUMBER: 1101 179
 TELEPHONE: 212 790 1030
 TELEFAX: 212 790 1030
 TELETYPE: 212 790 1030
 TELEFAX: 212 790 1030
 TELETYPE: 212 790 1030

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ 1: 16
 SEQUENCE INFORMATION:
 LENGTH: 39 amino acid
 TYPE: amino acid
 STRANDEDNESS: single
 TOPIC: amino acid
 MOLECULE TYPE: amino acid
 IN 08 189 341 5

Query Match 1.44 Score 67.76 Length 392
 Best Local Similarity 100.00 Prod. No. 992
 Matched 67.76 of 100.00 of Mismatches 02 Indels 02 Gaps 02

QY 88 PBLAF 34
 DB 19 PBLAF 34

RESULT 55
 IN 08 471 902A 5
 SEQUENCE 5, Application 108/4471902A

Patent No. 5646744
 GENERAL INFORMATION:
 APPLICANT: Foy, B. K.
 TITLE OF INVENTION: Polarity of amino acid
 NUMBER OF SEQUENCES: 16
 CORRESPONDENT ADDRESS:
 ADDRESS: Pennix & Edwards
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036 2711

COMPUTER: IBM PC compatible
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent in Release #10, Version #1.06
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 108/4471902A
 FILING DATE: 06 JUN 1995
 CLASSIFICATION: 540
 ATTORNEY/AGENT INFORMATION:
 NAME: Misko, S. Joseph
 REGISTRATION NUMBER: 18,872
 REFERENCE/AGENT NUMBER: 1101 179
 TELEPHONE: 212 790 1030
 TELEFAX: 212 790 1030
 TELETYPE: 212 790 1030
 TELEFAX: 212 790 1030
 TELETYPE: 212 790 1030

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ 1: 16
 SEQUENCE INFORMATION:
 LENGTH: 39 amino acid
 TYPE: amino acid
 STRANDEDNESS: single
 TOPIC: amino acid
 MOLECULE TYPE: amino acid
 IN 08 471 902A 5

NAME: MISTROCK, S. Leslie
REGISTRATION NUMBER: 19,872
REFERENCE/DOCKET NUMBER: 1101-143
TELECOMMUNICATION INFORMATION
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS
LENGTH: 38 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-471-800-5

Query Match 14%, Score 6, TP 0, Length 38,
Best Local Similarity 100.0%, Pred. No. 99,
Matches 6, Conservative 0, Mismatch 0, Indels 0

CY 88 FOLSAF 93
LB 13 FOLSAF 24

RESULT 56
US-08-471-800-5
Sequence 5, Application US/08471800
Patent No. 5852157
GENERAL INFORMATION
APPLICANT: KAY, B. K.
APPLICANT: FOWLES, D. M.
TITLE OF INVENTION: Tetraly Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS
ADDRESSEE: Pennie & Edmonds
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036 2711
COMPUTER READABLE FORM
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Polase #10, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08471800
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/113,416
FILING DATE
ATTORNEY/AGENT INFORMATION
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 19,872
REFERENCE/DOCKET NUMBER: 1101-143
TELECOMMUNICATION INFORMATION
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS
LENGTH: 38 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-471-800-5

Query Match 14%, Score 6, TP 0, Length 38,
Best Local Similarity 100.0%, Pred. No. 99,
Matches 6, Conservative 0, Mismatch 0, Indels 0

CY 88 FOLSAF 93
LB 13 FOLSAF 24

RESULT 57
US-08-471-068-5
Sequence 5, Application US/08471068
Patent No. 5841716
GENERAL INFORMATION
APPLICANT: KAY, B. K.
APPLICANT: FOWLES, D. M.
TITLE OF INVENTION: Tetraly Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS
ADDRESSEE: Pennie & Edmonds
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036 2711
COMPUTER READABLE FORM
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Polase #10, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08471068
FILING DATE
CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/113,331
FILING DATE
ATTORNEY/AGENT INFORMATION
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 19,872
REFERENCE/DOCKET NUMBER: 1101-143
TELECOMMUNICATION INFORMATION
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS
LENGTH: 38 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-471-068-5

Query Match 14%, Score 6, TP 0, Length 38,
Best Local Similarity 100.0%, Pred. No. 99,
Matches 6, Conservative 0, Mismatch 0, Indels 0

CY 88 FOLSAF 93
LB 13 FOLSAF 24

RESULT 58
US-08-706-3440-7
Sequence 5, Application US/087063440
Patent No. 6249555
GENERAL INFORMATION
APPLICANT: MASCO, WILMA
TITLE OF INVENTION: Genetic Alterations Related to Familial
TITLE OF INVENTION: Alzheimer's Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS
ADDRESSEE: Pennie & Edmonds
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036 2711
COMPUTER READABLE FORM
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Polase #10, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/087063440
FILING DATE
CLASSIFICATION: 435
PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/113,331
FILING DATE
ATTORNEY/AGENT INFORMATION
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 19,872
REFERENCE/DOCKET NUMBER: 1101-143
TELECOMMUNICATION INFORMATION
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS
LENGTH: 38 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: Peptide
US-08-706-3440-7

CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20004
 COMPUTER REARANGE P RM
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC COMP AT 100
 OPERATING SYSTEM: IBM PC COMP AT 100
 SOFTWARE: PATENT RELEASE #113, Version #1.03
 CURRENT APPLICATION DATA
 APPLICATION NUMBER: 1008/200,444
 FILING DATE: 30 APR 1996
 CLASSIFICATION: 300
 PRIOR APPLICATION DATA
 APPLICATION NUMBER: 6,700,004
 FILING DATE: 01 AUG 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: KIM, JUDITH D.
 REGISTRATION NUMBER: 41,671
 REFERENCE/ORDER NUMBER: 0007,414000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202,311,126
 TELEFAX: 202,311,126
 INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not provided
 MOLECULE TYPE: peptide
 ID: 09-905-744b-6

Query Match 1.431 Score 62 DB 42 Length 48
 Best Local Similarity 100.0% Prod. No. 02
 Matches 62 Conservative 02 Mismatches 02 Gaps 02

CY 1 100% 100%
 DB 1 100% 100%

RESULT 01
 US-09-905-744b-6
 Sequence 101, Application 1008/200,444
 Patent No. 6,700,004
 GENERAL INFORMATION:
 APPLICANT: KIM, JUDITH D.
 TITLE OF INVENTION: PATENT RELEASE #113, Version #1.03
 TITLE OF INVENTION: PATENT RELEASE #113, Version #1.03
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kim, Judith D.
 STREET: 420, Executive Square, Suite 440
 CITY: Washington
 STATE: DC
 ZIP: 20004
 TELEPHONE: 202,311,126
 TELEFAX: 202,311,126
 INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: not provided
 MOLECULE TYPE: peptide
 ID: 09-905-744b-6

TELEPHONE: (619) 678-5077
 TELEFAX: (619) 678-5098
 TELEX:
 INFORMATION FOR SEQ ID NO: 1
 SEQUENCE CHARACTERISTICS:
 LENGTH: 48 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ID: 09-905-744b-6

Query Match 1.431 Score 62 DB 42 Length 48
 Best Local Similarity 100.0% Prod. No. 02
 Matches 62 Conservative 02 Mismatches 02 Gaps 02

CY 251 100% 100%
 DB 6 100% 100%

RESULT 02
 US-09-905-744b-6
 Sequence 3, Application 1008/200,444
 Patent No. 6,700,004
 GENERAL INFORMATION:
 APPLICANT: KIM, JUDITH D.
 TITLE OF INVENTION: PATENT RELEASE #113, Version #1.03
 TITLE OF INVENTION: PATENT RELEASE #113, Version #1.03
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kim, Judith D.
 STREET: 420, Executive Square, Suite 440
 CITY: Washington
 STATE: DC
 ZIP: 20004
 TELEPHONE: 202,311,126
 TELEFAX: 202,311,126
 INFORMATION FOR SEQ ID NO: 3
 SEQUENCE CHARACTERISTICS:
 LENGTH: 62 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ID: 09-905-744b-6

Query Match 1.431 Score 62 DB 42 Length 48
 Best Local Similarity 100.0% Prod. No. 02
 Matches 62 Conservative 02 Mismatches 02 Gaps 02

CY 369 100% 100%
 DB 32 100% 100%

RESULT 01

US-09-511-485-16
 Sequence 16, Application US/090511485
 Patent No. 6292912
 GENERAL INFORMATION
 APPLICANT: KOTENOK, Peter G.
 APPLICANT: Mackenzie, Alexander E.
 APPLICANT: Baird, Stephen
 TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY PRIMERS,
 TIME OF INVENTION: PRIOR, AND INVENTION METHOD
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09-0511485
 FILING DATE: 04 AUG-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 09-040/000001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-4906
 TELEX: 200154
 INFORMATION FOR SEQ. 16 NO. 16
 SEQUENCE CHARACTERISTICS
 LENGTH: 68 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: both
 MOLECULE TYPE: protein
 US-09-511-485-16
 Query Match 14% Score 67 OF 67 Length 64
 Best Local Similarity 100.0% Freq No. 1 To 62
 Matches 67 Conservative 0, Mismatches 0, Indels 0, Gaps 0
 QY 43 VSASTL 48
 DQ 17 VSASTL 22
 RESULT 62
 US-09-511-485-17
 Sequence 17, Application US/090511485
 Patent No. 6292912
 GENERAL INFORMATION
 APPLICANT: KOTENOK, Peter G.
 APPLICANT: Mackenzie, Alexander E.
 APPLICANT: Baird, Stephen
 TITLE OF INVENTION: MAMMALIAN TAP GENE FAMILY PRIMERS,
 TIME OF INVENTION: PRIOR, AND INVENTION METHOD
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09-0511485
 FILING DATE: 04-AUG-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 09-040/000001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-4906
 TELEX: 200154
 INFORMATION FOR SEQ. 17 NO. 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 68 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: both
 MOLECULE TYPE: protein
 US-09-511-485-17
 Query Match 14% Score 67 OF 67 Length 64
 Best Local Similarity 100.0% Freq. No. 1 To 62
 Matches 67 Conservative 0, Mismatches 0, Indels 0, Gaps 0
 QY 43 VSASTL 48
 DQ 17 VSASTL 22
 RESULT 61
 US-09-091-725-27
 Sequence 27, Application US/0901725
 Patent No. 629141
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: 11-mer and 12-mer DNA for use in...
 TIME OF INVENTION: and recombinant DNA for use in...
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster LLP
 STREET: 2000 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: United States of America
 ZIP: 20006-1089
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.05 (EPV)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09-09091725
 FILING DATE: 23-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95003600.0
 FILING DATE: 23-DEC-1995
 APPLICATION NUMBER: EP 95003602.0
 FILING DATE: 11-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: E. Victor Donahue
 REGISTRATION NUMBER: 35,402
 INFORMATION FOR SEQ. 18 NO. 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 73 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-091-725-27


```

APPLICANT: Baylin, Stephen B.
APPLICANT: Wales, Michele M.
TITLE OF INVENTION: P-28,347
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 4000 Executive Plaza, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
CIF: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
SERIALS SYSTEM: F000000000
SOFTWARE: Patent Release #10, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/452,427
FILING DATE: 26-May-1995
CLASSIFICATION: 455
PRIORITY INFORMATION DATA:
APPLICATION NUMBER: 09/09740,003
FILING DATE: 15-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: P-28,347
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
SPARSENESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-452-427-7

Query Match
Best Local Similarity: 14%; Score 6; DB 2; Length 104;
Matches 6; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
OY 305 AEWLV 310
DI 06 AEWLV 101

RESULT 70
US-09-085-407-7
Sequence 7, Application: 09/09740,003
Patent No. 6103877
GENERAL INFORMATION:
APPLICANT: Baylin, Stephen B.
APPLICANT: Wales, Michele M.
TITLE OF INVENTION: NIVEL TUMOR SUPPRESSOR GENE, NUC-1
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 4000 Executive Plaza, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
CIF: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
SERIALS SYSTEM: F000000000
SOFTWARE: Patent Release #10, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/452,427
FILING DATE: 26-May-1995
CLASSIFICATION:

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PRIORITY INFORMATION DATA:
APPLICATION NUMBER: US/08/340,203
FILING DATE: 15 NOV 1994
ATTORNEY/AGENT INFORMATION:
NAME: Hallie, Ph.D., Lisa A.
REGISTRATION NUMBER: P-28,347
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
SPARSENESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-452-427-7

Query Match
Best Local Similarity: 14%; Score 6; DB 2; Length 104;
Matches 6; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
OY 305 AEWLV 310
DI 06 AEWLV 101

RESULT 71
US-09-395-689-3
Sequence 7, Application: 09/09740,003
Patent No. 6103877
GENERAL INFORMATION:
APPLICANT: Hwang, Jauhang
APPLICANT: Hu, Cho-Pat
TITLE OF INVENTION: TIGRIS-1
CURRENT APPLICATION NUMBER: US/09/395,689
CURRENT FILING DATE: 1999-09-13
SOFTWARE: FASTED 101 Windows Version 4.0
SEQ ID NO: 3
LENGTH: 105
TYPE: PRT
MOLECULE TYPE: protein
US-09-395-689-3

Query Match
Best Local Similarity: 14%; Score 6; DB 2; Length 105;
Matches 6; Conservation 0; Mismatches 0; Indels 0; Gaps 0;
OY 149 KEIPK 154
DI 1 KEIPK 6

RESULT 72
US-09-142-469-5
Sequence 5, Application: 09/09740,003
Patent No. 6140094
GENERAL INFORMATION:
APPLICANT: LOFFLER, Fridolin
APPLICANT: KUNZ, Gerald
APPLICANT: KUNZ, Gerd
APPLICANT: SCHNEIDER, Bruno
APPLICANT: SCHNEIDER, Bruno
TITLE OF INVENTION: PROTEIN WITH ENDOPLASMIC ACTIVITY
FILE REFERENCE: 0.0200-056
CURRENT FILING DATE: 1998-09-08
CURRENT APPLICATION NUMBER: P01/EP97/00081

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